Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months According to the Pre Publication Rules, every patent application received by the United States from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Published_Applications_NA contains nucleic acid sequences; the search results will have the Two new databases have been created to hold the pre-published sequences:

Published_Applications_AA contains amino acid sequences; the search results will have the

extension .rapb.

requests that the changed application be published again. In such instances, the "1" at the end of application. The first 4 digits show the calendar year the application was published. The next 7 beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the digits represent when the application was published. This 7-digit number starts at zero at the application had been published. If the applicants submit changes to the application, they may Publication Number is US20021234567A1. The "US" indicates the application was a U.S. Each pre-published application is given a unique Publication Number. An example of a

Sequences in the PGPub database are public information; it is permissible to leave these

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January 10, 2003, 08:32:32; Search time 5.91304 Seconds (without alignments) 99.519 Million cell updates/sec
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                121
1 XNCCNGGCSSKXCRDHARCC 20
                                                                                                                                                                                           US-09-910-009A-211
                                                                                                                                                                                                                Perfect score:
Sequence:
                                                                                                                 Run on:
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3 and in	<u> </u>	2 5	23	14	16,		37,	13,	13,	42,	1, A	~	, ,	12.	4	6	4	53	40,	7	Sequence 18, Appl	4	٧,	, 4	17	Sequence 4, Appli	
QI	US-08-900-230-3	8	US-08-279-058B-23	-08-828-323-2	US-09-003-198A-14	US-09-003-198A-16	-80-	63	US-09-548-372D-13	US-09-548-367D-13	US-08-691-814B-42	US-08-599-556-1	PCT-US96-05262-2	US-08-599-556-7	PCT-US96-05262-12	US-08-586-165-4	US-08-460-529B-9	US-08-900-230-46	US-08-900-230-53	US-08-900-230-40	US-08-479-722B-2	PCT-US95-02251-18	US-07-668-648-4	US-08-429-998-4	US-08-431-333-4	US-08-991-862-17	PCT-US91-02321-4	
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Length	1417	2211	58	58	40	67	1345	1400	2088	2088	54	22	22	27	27	359	170	45	45	4	83	3	g	ď	on on	593	G)	
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Gaps

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Score 58; DB 4; Length 1417; Pred. No. 28; 0; Mismatches 9; Indels

47.98; 50.08;

Query Match
Best Local Similarity 50.0°
Matches 9; Conservative

Db δy

Sequence 6, Appli Sequence 13, Appli Sequence 2, Appli Sequence 2, Appli Sequence 20, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli	,	RECEPTORS AND
1 US-07-906-349A-6 1 US-08-092-115-4 1 US-08-092-115-13 2 US-08-502-104-2 3 US-08-013-780-2 2 US-08-508-761B-22 2 US-08-508-761B-22 2 US-08-917-931-10 4 US-09-285-502-10 4 US-09-087-1385A-10 4 US-09-08-740A-3 4 US-09-068-740A-3 4 US-09-068-740A-3 4 US-09-068-740A-3 8 US-09-08-740A-3 1 US-09-08-740A-3 1 US-09-08-740A-3 3 US-08-872-855-4 4 US-09-981-392-12	ALIGNMENTS)	NG GALANN GALR3 DF nericas N.230 1.C/JPW/ADM
38.4 801 38.0 29 38.0 109 38.0 109 38.0 162 38.0 162 38.0 162 38.0 162 38.0 162 38.0 162 38.0 162 38.0 162 38.0 1702 38.0 702 38.0 702 38.0 702 38.0 702		Lication 97 Arion: aard, Jon Bard, Jon Button: UUENCES: Cooper 85 Avenu 7 York 7 York 7 York 1. S.A. 1. S.A. 1. S.A. 1. Low 1. Lo
28 46.5 30 46.5 31 32 46 46 33 34 46 46 46 46 46 46 46 46 46 4		RESULT 1 US-08-900-230-3 Sequence 3, Applicatio 5 Datent No. 6329197 GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: TOMBER OF SEQUENCES CORRESPONDENCE ADDR ADDRESSEE: COOPE STREET: 1185 Ave CITY: New York COUNTRY: U.S.A. ZIP: 11036 STREET: 1187 COMPUTER READABLE F PLO COMPUTER READABLE F PLO COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: DATENT TELEO MANICATION NUMBE FILING DATE: 23- CLASSIFICATION NUMBE FILING DATE: 31- CLASSIFICATION NUMBE FILING DATE: TOP REFERENCE/COCKET INFO NAME: White, John REGISTRATION NUMBE FILECOMMUNICATION II TELEPHONE: 212-39-1 INFORMATION FOR SEQ II SEQUENCE CHARACTERI LENGTH: 1417 amin acid STRANDENESS: SII TYPE: amino acid STRANDENESS: SII TYPE: amino acid STRANDENESS: SII TYPE: ANTI-SERSE: NO ANTI-SERSE: NO
		B none of the contract of the

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Sequence 1, Application US/09738884
; Sequence 1, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
    APPLICANT: GUECLER. Karl et al
    TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
    TITLE OF INVENTION: PROTEINS, AND USES THEREOF
    TITLE OF INVENTION: PROTEINS, AND USES THEREOF
    TITLE OF INVENTION: NUMBER: US/09/738,884
    CURRENT APPLICATION NUMBER: US/09/738,884
    CURRENT FILING DATE: 2000-12-18
    NUMBER OF SEQ ID NOS: 5
    SOFTWARE: FastSEQ for Mindows Version 4.0
    SEQ ID NO 1
    LENCTH: 2211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: MICHAEL E. O'DONNELL
TITLE OF INVENTION: HOLDENZME
TITLE OF INVENTION: HOLDENZME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 SKytop Drive
CITY: Trumbull
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRF D-1056CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,058B
FILING DATE:
CLASSIFICATION: 435
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Patent No. 5668004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF I
TELECOMMUNICATION INFORMATION:
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.6%;
47.1%;
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50.08;
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CCNGGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 CCCGGCTCCGCAAGATCC 64
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Matches 9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Human
US-09-738-884-1
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RESULT 2
US-09-738-884-1
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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APPLICANT: Shah, Dilip Maganlal
APPLICANT: W. Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 4; Length 58;
Pred. No. 5.4;
2; Mismatches 7; Indels
   7; Indels
                                                                                                                                                                                                                  GENERAL INFORMATION: Michael
TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME
FILE REPERENCE: 1960/3/10214
CURRENT PELING DATE: 1997-03-28
CURRENT FILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 58
ILENGTH: 58
TYPE: PRT
CORGANISM: Escherichia coli
US-08-928-323-23
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09003198A Patent No. 6316407
                                                                                                                                                              ; Sequence 23, Application US/08828323A
; Patent No. 6413753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CNGGCSSKXCRDHARCC 20
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                                         4 CNGGCSSKXCRDHARCC 20
                                                                1 |||:: | | |||
38 CTGGCTACTCGTGAACC 54
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       8; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-09-003-198A-14
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                                                                                                                                                    US-08-828-323-23
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         Matches
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RESULT 8
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US-09-003-198A-16
Sequence 16, Application US/09003198A
Sequence 16, Application US/09003198A
Sequence 16, Application US/09003198A
Setent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                          43.8%; Score 53; DB 4; Length 40; 40.7%; Pred. No. 5.1; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%; Score 53; DB 4; Length 67; 40.7%; Pred. No. 7.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEDEHONE: (713) 787-1440
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                            4 CNGGCS-----SKXCRDHARCC 20
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Patent No. 5972684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                        Query Match
Best Local Similarity 40.7%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 67 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 40.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.O. Box 4433
              STRANDEDNESS:
TOPOLOGY: linear
US-09-003-198A-14
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: Linear
US-09-003-198A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-977-767-3
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APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, NO. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: KOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.4%; Score 52.5; DB 2; 50.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                             SOFTWARE: FASTEM: DOS SOFTWARE: FASTES for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977.767
                                  APPLICANT: Corley, Neil C.
TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0423 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/08630915A Patent No. 6309820 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1345 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CCNGGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                               Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650-855-05
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: single
linear
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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 Yue, Henry
Greenwald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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IMMEDIATE SOURCE:
LIBRARY: GenBan
CLONE: 1532042
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                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                               COUNTRY: U. ZIP: 94304
                                                                                                                                                                CA
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-977-767-3
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APPLICANTS GURNEY AL.

APPLICANTS GURNEY AL.

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 29915/6280H

CURRENT APPLICATION NUMBER: US/09/548,367D

CURRENT FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 73

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1
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Patent No. 5981218
GENERAL INFORMATION:
APPLICANT: Rio, Marie-Christine
APPLICANT: Basset, Paul
APPLICANT: Basset, Paul
APPLICANT: Byrne, Jennifer
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 10; Indels
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MEDIUM TYPE: Floppy disk
GOMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
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APPLICATION NUMBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
Sequence 13, Application US/09548367D Patent No. 6440698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 136
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEO ID NO: 42:
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ORGANISM: Homo sapiens
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STATE: DC
COUNTRY: USA
TO 20005-3934
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                                                       GENERAL INFORMATION:
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APPLICANT: GURREY ET AL.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.3%; Score 50; DB 4; Length 2088; 44.4%; Pred. No. 2.9e+02; tive 0; Mismatches 10; Indels
                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 29915/62801

FILE REFERENCE: 29915/62801

CURRENT APPLICATION NUMBER: US,09/548,372D

CURRENT FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: US,60/155,493

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1998-09-23

PRIOR FILING DATE: 1998-09-24
                                                                                                                                              APPLICATION NUMBER: US/08/630,915A FILING DATE: 03-APR-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                    1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09548372D Patent No. 6420534
                                                                                                                                                                                                                    ATTORNEY INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-1
TELECHONE: (212) 790-9090
TELEPAN: (212) 869-8864/9741
TELEX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 maino acids
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1617 CCTGGACGATCTCCAGCC 1634
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Best Local Similarity 44.45
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 43.49
Best Local Similarity 50.09
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: DNA US-08-630-915A-37
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US-09-548-367D-13
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US-09-548-372D-13
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LENGTH: 2088
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amino acid
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               NAME/KEY:
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                                   LOCATION:
                                                                                   LOCATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                      Gaps
                                                                                                                                                                    1;
                                                                                                                                    DB 2; Length 54;
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Shon, Ki-Joon
APPLICANT: Yoshikami, Doju
APPLICANT: Marsh, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Conctoxin Peptide PIIIA
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 24260-107674-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
                                                                                                                                                                    1; Mismatches
                                                                                                                                  Score 49.5; |
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/599,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08599556
Patent No. 5670622
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38,609
                                      TOPOLOGY: not relevant MOLECULE TYPE: peptide
                                                                                                                                  40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                      3 CCNGGCSSKXCRDHARCC 20
                                                                                                                                                                                                                         25 CCHGGCISPSIA-HGRLC 41
                                                                                                                  Ouery Match
Best Local Similarity 50.vv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Saxe, Stephen A. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 amino acids
               54 amino acids
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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OPERATING SYSTEM:
                                 TYPE: amino acid
STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20005-3917
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                                                                                                 US-08-691-814B-42
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/product= "OTHER"
/note= "Amino acid 18 is 4-transhydroxyproline or proline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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/note= "The carboxy terminus may be amidated.
                                                                                                                                                                                                                                                                                                                                                                                                                       40.1%; Score 48.5; DB 1; Length 22; 45.0%; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Venable, Baetjer, Howard & Civiletti, LLP
1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/05262 FILING DATE: 17-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24260-107674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yoshikami, Doju
APPLICANT: Marsh, Maren
APPLICANT: Gruz, Lourdes J.
APPLICANT: Hillyard, David R.
TITLE OF INVENTION: Conctoxin Peptides
UNMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 17-APR-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/423,561
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
PCT-0S96-05262-2
Sequence 2, Application PC/TUS9605262
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shon, Ki-Joon
Grilley, Michelle M.
Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CCN--GGCSSKXCRDHARCC 20
Disulfide-bond
                                                             Disulfide-bond
                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202-962-4848
                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CCGFXKSCRSRQCKXH-RCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Saxe, Stephen A. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202-962-8300
                                                                                                                                                                                                        LOCATION: 18
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                COCATION: 22
CTHER INFORMATION:
CTHER INFORMATION:
US-08-599-556-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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Gaps

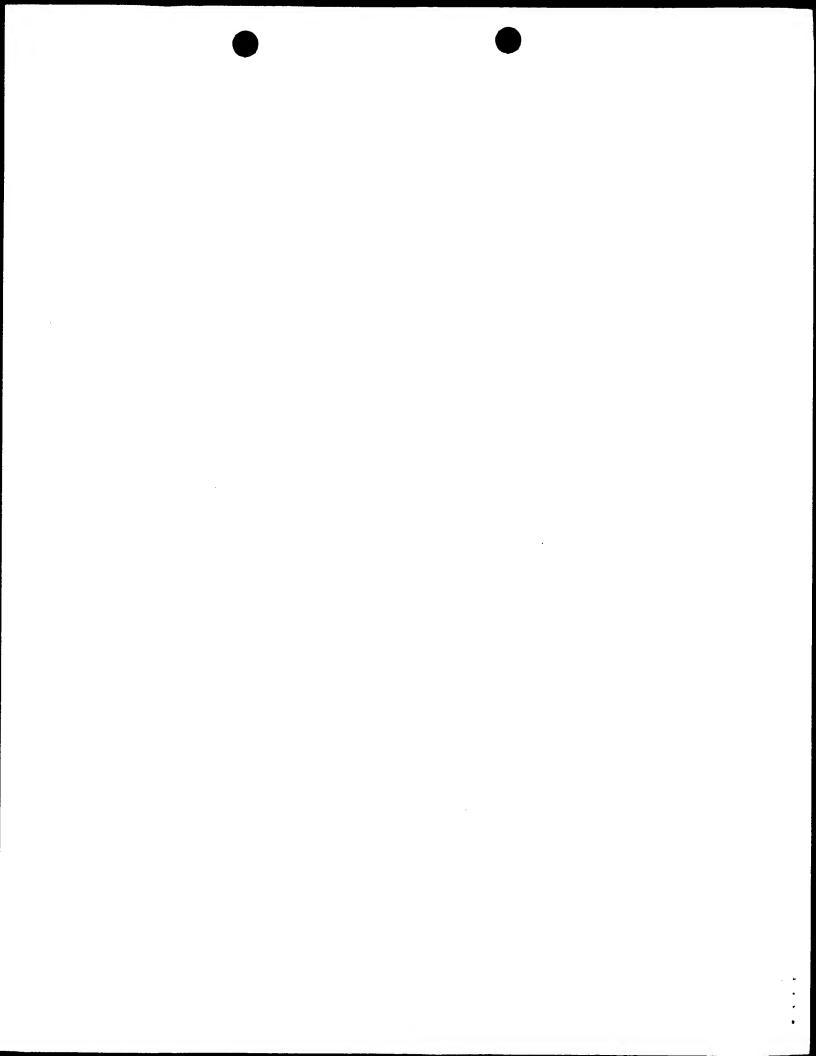
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DB 1; Length 27;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .B: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                             24260-107674-03
                                                                                                                                                                                                                                                                                                                                       40.1%; Score 48.5; D
45.0%; Pred. No. 12;
tive 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marsh, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
TITLE OF INVENTION: Conotoxin Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: PCT/US96/05262
17-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/423,561
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application PC/TUS9605262
GENERAL INFORMATION:
APPLICANT: Shon, Ki-Joon
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SARA, Stephen A:
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2426(
TELEPHONE: 202-96-4848
TELEPHONE: 202-96-4848
TELEFAX: 202-96-4830
: INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grilley, Michelle M.
Olivera, Baldomero M.
Yoshikami, Doju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38,609
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 3 CCN--GGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CCGFPKSCRSRQCKPH-RCC 25
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LENGTH: 27 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Saxe, Stephen A. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202 CO. TELEPHONE: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein PCT-US96-05262-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: LZVI
TTY: Washington
                                                                                                                                                                                                                                             amino acid
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PCT-US96-05262-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                    US-08-599-556-7
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                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acid 18 is 4-trans-hydroxyproline or proline."
                                                                                                                                                                                                                                                                                                    /note= "Amino acid 8 is 4-trans-hydroxyproline or proline."
                                                                                                                                                                     LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Amino acid 1 is pyroglutamate or glutamine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "OTHER"
/note= "The carboxy terminus may be amidated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.1%; Score 48.5; DB 5; Length 22; 45.0%; Pred. No. 9.8; tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005-3917
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Shon, Ki-Joon
APPLICANT: OSSHikami, Doju
APPLICANT: Marsh, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Conctoxin Peptide PIIIA
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /product= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /product= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/599,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08599556
Patent No. 5670622
                                                                                                               ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CCN--GGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CCGFXKSCRSRQCKXH-RCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
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18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                    NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.0 Matches 9; Conservative
                           TOPOLOGY: Illicar
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                     STRANDEDNESS: single
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                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
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LOCATION:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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STATE: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US96-05262-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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5
Query Match 40.1%; Score 48.5; DB 5; Length 27; Best Local Similarity 45.0%; Pred. No. 12; Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps
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qq

Search completed: January 10, 2003, 08:38:18 Job time : 7.91304 secs



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January 10, 2003, 08:33:07; Search time 30.9565 Seconds (without alignments) 12.534 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118974 seqs, 19401057 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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121
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                         Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 24, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 37, Appl	Sequence 451, App	Sequence 3, Appli	Sequence 269, App	Sequence 1, Appli	Sequence 581, App	Sequence 9, Appli	Sequence 114, App	Seguence 19, Appl	Sequence 58, Appl	Sequence 105, App	Sequence 407, App	Seguence 426, App	Sequence 428, App
	. di	US-10-029-217A-24	US-09-060-854B-2	US-10-096-961-1	US-09-826-508-3	US-09-804-898-2	US-09-879-957-37	US-10-052-586-451	US-08-969-137-3	US-10-052-586-269	US-09-735-933-1	US-10-052-586-581	US-09-361-736-9	US-09-749-637A-114	US-09-894-882-19	US-09-894-882-58	US-09-894-882-105	US-09-894-882-407	US-09-894-882-426	US-09-894-882-428
	DB	. 6	10	6	10	10	10	12	æ	12	10	. 12	10	6	10	10	10	10	10	10
	Length DB	3907	1497	2211	1200	4679	1400	1743	42	1300	1422	1435	170	26	46	46	46	46	46	46
æ	Query Match	48.8	47.1	47.1	45.5	44.2	43.4	42.1	41.3	41.3	41.3	40.5	39.7	38.8	38.8	38.8	38.8	38.8	38.8	38.8
	Score	59	57	57	55	53.5	52.5	51	20	20	20	49	48	47	47	47	47	47	47	47
	Result No.		2	e	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

Sequence 28, Appl Sequence 431, App	Sequence 18, Appl	Sequence 57, Appl	Sequence 104, App	Sequence 27, Appl	Sequence 431, App	Sequence 17, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 1416, Ap	Sequence 97, Appl	Sequence 87, Appl	Sequence 93, Appl	Sequence 1686, Ap	Sequence 10, Appl	Sequence 2, Appli	Sequence 50, Appl	Sequence 3, Appli	Sequence 4, Appli	Sequence 20, Appl	Sequence 346, App	Sequence 21, Appl	Sequence 9, Appli	Sequence 47, Appl	Sequence 518, App
US-09-894-882-28 US-09-894-882-431	US-09-894-882-18	US-09-894-882-57	US-09-894-882-104	US-09-894-882-27	US-09-886-055-431	US-09-824-647-17	US-09-813-156-17	US-09-824-807-17	US-09-925-301-1416	US-10-052-586-97	US-09-894-882-87	US-09-894-882-93	US-09-925-300-1686	US-09-871-388-10	US-09-995-593A-2	US-09-764-903-50	US-09-995-593A-3	US-09-995-593A-4	US-09-756-071B-20	US-10-028-072-346	US-09-828-366-21	US-09-995-593A-9	US-09-975-143-47	US-10-052-586-518
10	10	10	10	10	10	σ	10	10	10	12	10	10	10		10		10		10	6	10	10	6	12
4 4 8	82	82	82	84	975	593	593	593	621	1894	40	40	141	162	200	252	520	702	720	723	723	723	914	1137
38.8 38.8	38.8	38.8	38.8	38.8	38.8	38.4	38.4	38.4	38.4	38.4	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	α	œ	38.0	œ	œ	38.0
47	47	47	47	47	47	46.5	46.5	46.5	46.5	46.5	46	46	46	46	46	46	46	46	46	46	46	46	46	46
20 21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMEN

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Sequence 2, Application US/09060854B
Patent No. US20020081703A1
GENERAL INFORMATION:
APPLICANT: Estell, David Aaron
TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. US2002
TITLE OF INVENTION: Proteins
FILE REFERENCE: GC532
                              Sequence 24, Application US/10029217A

Sequence 24, Application US/10029217A

Patent No. US20020164735A1

GENERAL INFORMATION:

APPLICANT: OLSON, ENC N.

TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC

TITLE OF INVENTION: MCLEAR REGULATORY FACTOR

FILE REFERENCE: UTSD:695US

CURRENT TILING DATE: 2002-03-19

PRIOR PILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 32

SEQ ID NO 24

LENGTH: 3907
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44.4%; Pred. No. 20;
tive 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/060,854B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 CCTGGCAGAGCAGCCTCC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CCNGGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus US-10-029-217A-24
RESULT 1
US-10-029-217A-24
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Sequence 1, Application US/10096961
; Sequence 1, Application US/10096961
; Sequence 1, Application US/200201555221
; GENERAL INFORMATION:
; APPLICANF: GUBGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REPREMENCE: CLOO03491DV
; CURRENT APPLICATION NUMBER: US/20/96,961
; PRIOR APPLICATION NUMBER: US/232,632
; PRIOR APPLICATION NUMBER: 09/738,884
; PRIOR FILING DATE: 2000-10-14
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2211
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Patent No. US20010025099A1
GENERAL INFORMATION:
APPLICANT: Nabil Elshourbagy
TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
TITLE OF INVENTION: G Protein-Coupled Secoptor Polypeptides
TITLE OF INVENTION: G Protein-Coupled Secoptor Polypeptides
CURRENT APPLICATION NUMBER: US/09/826,508
CURRENT APPLICATION NUMBER: US/09/826,508
NUMBER OF SEC ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                               Score 57; DB 10; Length 1497; Pred. No. 16; 1; Mismatches 6; Indels
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Pred. No. 22;
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CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                        TYPE: PRT ORGANISM: B. amyloliquefaciens
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50.0%;
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50.0%;
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Best Local Similarity 50.08
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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CORGANISM: HOMO SAPIENS
US-09-826-508-3
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Best Local Similarity
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Best Local Similarity
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                                                                                        LENGTH: 1497
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US-09-826-508-3
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US-10-096-961-1
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FOWLKES, Dana M.
MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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9; Indels
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                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: DURING, MATTHEM
APPLICANT: XIAO, WEIDONG
AITLE OF INVENTION: PRODUCTION OF CHIMERIC CAPSID VECTORS
FILE REFERENCE: 102182-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.2%; Score 53.5; C
44.4%; Pred. No. 96;
tive 2; Mismatches
Mismatches
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                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/804,898
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/189,110
PRIOR FILING DATE: 2000-03-14
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REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37, Application US/09879957 Patent No. US20020034755A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: adeno-associated virus 2
                                                                                                                                                                US-09-804-898-2; Sequence 2, Application US/09804898; Patent No. US20020045264A1
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                       3 CCNGGCSSKXCRDHARCC 20
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                                                                                 40 CCGGGCAGGTCCGCGCC 57
8; Conservative
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4679
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  Matches
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C1 CURRENT APPLICATION NUMBER: US/10/052,586
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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43.4%; Score 52.5; DB 10; Length 1400;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 9; Conservative 1; Mismatches 5; Indels 3;
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID NO: 37: US-09-879-957-37
                                                TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
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PRIOR APPLICATION NUMBER: 60/059263
PRIOR FLING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/063120
PRIOR APPLICATION NUMBER: 60/063121
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
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PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR APPLICATION NUMBER: 60/063564
PRIOR APPLICATION NUMBER: 60/063564
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 451, Application US/10052586 Patent No. US20020127584A1 GENERAL INFORMATION:
                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                           LENGTH: 1400 amino acids
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PRIOR APPLICATION NUMBER: 60/063870
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FILING DATE: 1997-11-13
                                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 CCGGGCA---CTGTACCC 204
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                                                                                                                                                                                                         TYPE: amino acid
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Gurney, Austin L.
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Smith, Victoria
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PAPLICATION NUMBER: 60/080107
PRIOR PELING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR APPLICATION NUMBER: 60/08037
PRIOR PILING DATE: 1998-04-01
PRIOR PELING DATE: 1998-04-01
PRIOR PELING DATE: 1998-04-01
PRIOR PELING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081070
PRIOR APPLICATION NUMBER: 60/081070
PRIOR APPLICATION NUMBER: 60/081070
PRIOR APPLICATION NUMBER: 60/081070
PRIOR APPLICATION NUMBER: 60/081195
PRIOR PELING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/08138
PRIOR APPLICATION NUMBER: 60/081838
PRIOR APPLICATION NUMBER: 60/081838
PRIOR PELING DATE: 1998-04-15
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
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APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1000 A.C.
                                                                                                                                                                                                    FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069425
FILING DATE: 1997-12-12
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FILING DATE: 1997-12-17
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APPLICATION NUMBER: 60/068017
FILING DATE: 1997-12-18
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PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/083496
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PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/066466
                              FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066772
                                                                                                                                                                 APPLICATION NUMBER: 60/069335
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FILING DATE: 1998-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/083495
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                                                                                                                     1997-11-24
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APPLICATION NUMBER:
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                              PRIOR PRIOR
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085599
PRIOR APPLICATION NUMBER: 60/085582
PRIOR APLICATION NUMBER: 60/085582
PRIOR PLILING DATE: 1998-05-15
PRIOR PLILING DATE: 1998-05-12
PRIOR PLILING DATE: 1998-05-22
PRIOR PLILING DATE: 1998-05-22
PRIOR PLILING DATE: 1998-05-02
PRIOR APPLICATION NUMBER: 60/08769
PRIOR PLILING DATE: 1998-06-02
PRIOR PLILING DATE: 1998-06-02
PRIOR PLILING DATE: 1998-06-03
PRIOR PLILING DATE: 1998-06-03
PRIOR PLILING DATE: 1998-06-04
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-07
PRIOR PLILING DATE: 1998-06-07
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-07
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-11
PRIOR PLILOR DATE: 1998-06-11
PRIOR PLILING D
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FILING DATE: 1998-06-16
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GENERAL INFORMATION:
APPLICANT: KANDEL, ERIC
APPLICANT: MAYEORD, MARK
TITLE OF INVENTION: DNA REGULATORY ELEMENT FOR THE
TITLE OF INVENTION: EXPRESSION OF TRANSGENES IN NEURONS OF THE MOUSE FOREBRAIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER AND DUNHAM
                                                                                                                                                                                              Gaps
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                                                                                                                                                        Score 51; DB 12; Length 1743; Pred. No. 83;
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                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/969,137 FILING DATE: 12-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 8
Pred. No. 5.5;
2; Mismatches
                                                                                                                                                                                                1; Mismatches
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CITY: NEW YORK
COUNTRY: UNITED STATE:

ZIP: 10036
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ER: 0575/52776
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR APPLICATION NUMBER: 60/08953
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR PLICATION NUMBER: 60/089908
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; Patent No. US20020127584A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    US-08-969-137-3
; Sequence 3, Application US/08969137
; Patent No. US20010018207A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-NOV-1997
CLASSIFICATION: 800
ATTORNEY/GENT INFORMATION:
NAME: WHITE, JOHN P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 057:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.38;
44.48;
                                                                                                                                                            42.18;
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TELEFAX: (212)3910525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212)3910525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            Query Match 42.19
Best Local Similarity 44.45
Matches 8; Conservative
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Best Local Similarity 44.4
Matches 8; Conservative
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US-08-969-137-3
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C1
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/05256
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PLING DATE: 1997-00-24
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063121
PRIOR APPLICATION NUMBER: 60/063121
PRIOR APPLICATION NUMBER: 60/063121
PRIOR PRILING DATE: 1997-10-24
PRIOR PRILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR PILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR APPLICATION NUMBER: 60/063734
PRIOR PILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR PILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063101
PRIOR APPLICATION NUMBER: 60/063101
PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066120
PRIOR PELING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066120
PRIOR APPLICATION NUMBER: 60/066120
PRIOR APPLICATION NUMBER: 60/06935
PRIOR APPLICATION NUMBER: 60/06937
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/0778986
PRIOR PILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: 60/0778986
PRIOR PILING DATE: 1998-03-11
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FILING DATE: 1938-03-20
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/080107
                                               Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                              Watanabe, Colin K.
Wood, William I.
                                                                                                                                                      Pan, James
Smith, Victoria
Baker, Kevin P.
                                                                                                                                                                                                                                                                   Zhang, Zemin
                           Chen, Jian
                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08 R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/083322
R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/083495
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083496 R APPLICATION NUMBER: 60/084414 R FILING DATE: 1998-05-06 R APLICATION NUMBER: 60/084639 R FILING DATE: 1998-05-07 R FILING DATE: 1998-05-07 R FILING DATE: 1998-05-07 R FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/083499 FILING DATE: 1998-04-29 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081070 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081838 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 PILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085700 FILING DATE: 1998-05-15 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/086486 FILING DATE: 1998-05-22 PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/081195 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/084366 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085573 APPLICATION NUMBER: 60/085579 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085582 APPLICATION NUMBER: 60/086023 FILLING DATE: 1998-05-18 APPLICATION NUMBER: 60/086392 PRIOR APPLICATION NUMBER: 60/087759 PRIOR FILING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 60/087827 PRIOR FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/085580 APPLICATION NUMBER: 60/087098 APPLICATION NUMBER: 60/087208 APPLICATION NUMBER: 60/087609 1998-04-08 FILING DATE: 1998-03-31 1998-05-05 FILING DATE: 1998-05-15 1998-05-15 .998-05-28 FILING DATE: 1998-05-28 1998-06-02 FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: PRIOR PRIOR

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FILING DATE: 1997-11-24
APPLICATION UNMBER: 60/066772
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/069335
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Watanabe, Colin K.
Wood, William I.
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Gurney, Austin L.
                                                                                                                                                                                                                                                                   Best_Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                          3 CCNGGCSSKXCRDHARC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-052-586-581
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APPLICANT:
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APPLICANT:
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                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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1; Mismatches
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR PAPLICATION NUMBER: 60/088167
PRIOR APPLICATION NUMBER: 60/088212
PRIOR APPLICATION NUMBER: 60/088212
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/08872
PRIOR PLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08825
PRIOR APPLICATION NUMBER: 60/088826
PRIOR PLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088861
PRIOR PLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088861
PRIOR PLING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR PLING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088961
PRIOR APPLICATION NUMBER: 60/088961
PRIOR APPLICATION NUMBER: 60/088961
PRIOR PLING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08990
PRIOR PLING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/0899105
PRIOR APPLICATION NUMBER: 60/0899105
PRIOR PRIOR DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/0899105
PRIOR APPLICATION NUMBER:
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PRIOR FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089653
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PRIOR APPLICATION NUMBER: 60/089908
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Patent No. US2002003034A1
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 CCTGGACATGCTGTCACC 542
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Best Local Similarity 38.99
Matches 7; Conservative
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US-09-735-933-1
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/10/052,586

CURRENT APPLICATION NUMBER: 00/05266

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR PRIOR APPLICATION NUMBER: 60/062250

PRIOR PRIOR APPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-28

PRIOR PILING DATE: 1997-10-29

PRIOR PILING DATE: 1997-10-31

PRIOR PILING DATE: 1997-10-31

PRIOR PILING DATE: 1997-10-31
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                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 581, Application US/10052586
; Patent No. US20020127584A1
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PRIOR APPLICATION NUMBER: 60/065311
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DR APPLICATION NUMBER: 60/069425
DR FILING DATE: 1997-12-12
DR APPLICATION NUMBER: 60/069870
DR FILING DATE: 1997-12-17
DR APPLICATION NUMBER: 60/068017
DR FILING DATE: 1997-12-18 FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085582
FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081838 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/084366 FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/083495 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083499 FILING DATE: 1998-04-29 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081070 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/083496 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/084414 APPLICATION NUMBER: 60/084639 APPLICATION NUMBER: 60/084640 APPLICATION NUMBER: 60/084643 APPLICATION NUMBER: 60/085573 APPLICATION NUMBER: 60/085579 APPLICATION NUMBER: 60/077632 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077649 APPLICATION NUMBER: 60/079664 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079786 APPLICATION NUMBER: 60/080107 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/081049 APPLICATION NUMBER: 60/082569 FILING DATE: 1997-12-18 APPLICATION NUMBER: 60/077450 APPLICATION NUMBER: 60/078886 APPLICATION NUMBER: 60/078939 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/080194 APPLICATION NUMBER: 60/080327 APPLICATION NUMBER: 60/080333 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-05-06 FILING DATE: 1998-05-07 FILING DATE: 1998-05-15 1998-03-20 1998-05-07 FILING DATE: 1998-03-10 FILING DATE: 1998-05-07 FILING DATE: 1997-12-11 1998-03-11 FILING DATE: 1998-03-31 FILING DATE: 1998-04-01 FILING DATE: 1998-04-01 FILING DATE: 1998-04-21 FILING DATE: 1998-04-21 FILING DATE: : FILING DATE: FILING DATE: PRIOR
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R APPLICATION NUMBER: 60/086392 R FILING DATE: 1998-05-22 R APPLICATION NUMBER: 60/086486 RR FILING DATE: 1998-05-22 R APPLICATION NUMBER: 60/087098 R APPLICATION NUMBER: 60/087208 R APPLICATION NUMBER: 60/087208 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088863 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 APPLICATION NUMBER: 60/08824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088825 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088861 918880/09 APPLICATION NUMBER: 60/089090 APPLICATION NUMBER: 60/089105 APPLICATION NUMBER: 60/089538 APPLICATION NUMBER: 60/089598 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/086023 FILING DATE: 1998-05-18 APPLICATION NUMBER: 60/087609 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087827 FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088655 APPLICATION NUMBER: 60/088722 APPLICATION NUMBER: 60/088738 APPLICATION NUMBER: 60/088740 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088811 APPLICATION NUMBER: 60/088826 APPLICATION NUMBER: 60/088029 APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: 60/088217 APPLICATION NUMBER: 60/085700 FILING DATE: 1998-06-09 FILING DATE: 1998-06-16 FILING DATE: 1998-06-04 1998-06-10 FILING DATE: 1998-06-10 ILING DATE: 1998-06-10 1998-06-12 1998-06-17 1998-06-17 1998-06-17 FILING DATE: 1998-06-04 ILING DATE: 1998-06-05 ILING DATE: 1998-06-05 FILING DATE: 1998-06-11 1998-06-11 APPLICATION NUMBER: FILING DATE: 1998-0 'ILING DATE: FILING DATE: FILING DATE: PRIOR PRIOR PRIOR PRIOR
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Score 49; DB 12; Length 1435;
Pred. No. 1.2e+02;
1; Mismatches 10; Indels (
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42.9%; Pred. No. 28;
tive 3; Mismatches 5; Indels
                                                                                                                                                                                                            Sequence 9, Application US/09361736
Patent No. US20020102634A1
GENERAL INFORMATION:
TITLE OF INVENTION: Human Stanniocalcin-alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Caltier, G. Edward
APPLICANT: Warkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325800-334 (PF143)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/460,529
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFRENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CCNG----GCSSKXCRDHARC 19
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERSTICS:
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                                                                                                                     232 CCTGGAAGAACCATGTCC 249
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AMINO ACID
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                                           Conservative
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Best Local Similarity 42.9
Matches 9; Conservative
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                      Best_Local Similarity
Matches 7; Conserva
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US-09-749-637A-114
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APPLICANT:
  Query Match
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PAPLICANT: HILTOCOME, J. Michael

APPLICANT: HOLICOME, J. Michael

APPLICANT: JOSES, ROBERT M.

PAPLICANT: JOSES, ROBERT M.

COURRENT PALICATION NUMBER: US 60/213,412

PRINCE PRINCE DATE: 2000-12/20/21/412

PRINCE DATE: 2
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) ORGANISM: Conus radiatus

) FEATURE:

) NAME/KEY: PEPTIDE

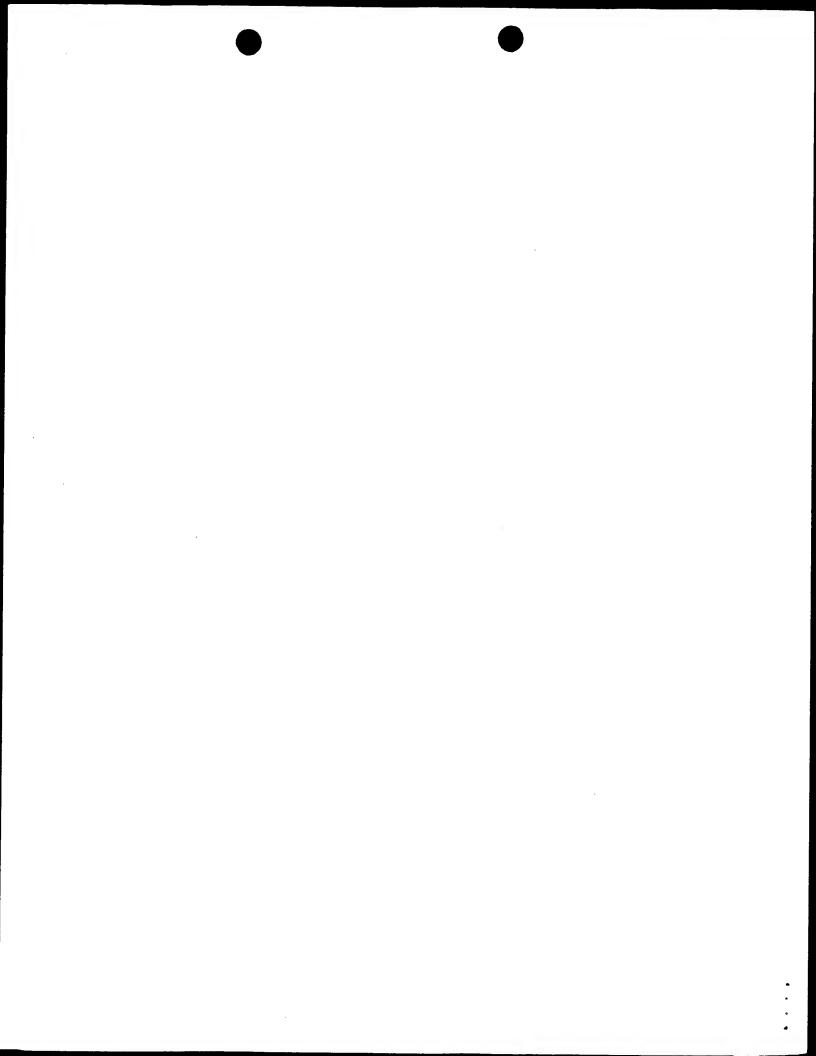
) LOCATION: (1)..(46)

) OTHER INFORMATION: Xaa at residues 4, 23, 29, 36 and 42 is Pro or hydroxy-Pro; Xaa

) OTHER INFORMATION: t residue 33 is Trp or bromo-Tr

US-09-894-882-19
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; LOCATION: (1)..(46)
; OTHER INFORMATION: Xaa at residues 4, 23, 29 and 36 is Pro or hydroxy-Pro
US-09-894-882-58
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38.8%; Score 47; DB 10; Length 46;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                           38.8%; Score 47; DB 10; Length 46; 50.0%; Pred. No. 13; tive 2; Mismatches 5; Indels
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sequence 58, Application US/09894882
sequence 58, Application US/09894882
sequence 58, Application US/09894882
setten No. US20020102607A1
setten No. US20020102607A1
septent No. US20020102607A1
septent No. Usersity of Utah Research Foundation
septentCaNT: Cognetix, Inc.
APPLICANT: Malker, Craig S.
APPLICANT: Jimenez, Elsie C.
APPLICANT: Jimenez, Baldomero M.
APPLICANT: Markins, Maren
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FUNENT FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/245,3410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PELING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PELING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO SED ID NOS: 506
LENGTH: 46
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Best Local Similarity 50.03
Matches 7; Conservative
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6 GKDGRQCRNHADCC 19
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US-09-894-882-58
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 10, 2003, 08:32:27; Search time 26.2609 Seconds (without alignments) 101.482 Million cell updates/sec Run on:

US-09-910-009A-432

134 1 ZNCCNGGCSSKWCRDHARCC 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters: seq length: 0 seq length: 2000000000 Minimum DB s Maximum DB s

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

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/SIDS2/gcdata/genescqq/genescqp_embL/AA1987.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1997 A_Geneseq_101002:* 112 :: 112 :: 114 :: 115 :: 116 :: 11 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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27-28-28-28-28-28-28-28-28-28-28-28-28-28-	
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88 8 3 3 4 5 8 8 3 3 5 8 8 3 5 8 8 8 8 8 8 8 8 8 8	00000000000000000000000000000000000000
11111111111111111111111111111111111111	39 441 443 445

ALIGNMENTS

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ABB88449 standard; Peptide; 20 AA.
                                                             ABB88449;
RESULT 1
                ABB88449
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C striatus mu-conopeptide SEQ ID NO: 432. (first entry)

24-MAY-2002

Mu-conopeptide; snail: venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antidajing; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.

Conus striatus.

WO200207678-A2

31-JAN-2002

23-JUL-2001; 2001WO-US23125

2000US-219619P 21-JUL-2000;

2000US-245157P. 2001US-264319P. 2001US-277270P 03-NOV-2000; 29-JAN-2001; 21-MAR-2001; 2

(UTAH) UNIV UTAH RES FOUND (COGN-) COGNETIX INC.

Shon K; Olivera BM, Mcintosh JM, Garrett JE, Watkins M, Cruz LJ, 2

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB88284
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                                                                                                                                                                    The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, pest-herpetic neuropath, in neuronal pain and phantom limb, burn pain, brain or spinal cord trauma, myocardial infarct, physical trauma, brain or spinal cord trauma, myocardial infarct, physical trauma, perhaptal as physia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                             New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M, Garrett JE, Watkins M, Cruz LJ, Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 134; DB 23; 100.0%; Pred. No. 3.1e-08;
   Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       striatus mu-conopeptide S3-2 propeptide.
      Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB88283 standard; Protein; 75 AA.
                                                                                                                                               Claim 1; Page 85; 231pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ZNCCNGGCSSKWCRDHARCC 20
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2000US-245157P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ZNCCNGGCSSKWCRDHARCC
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcintosh
    Jones RM,
                                                                                                               neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-217020/27.
                                    WPI; 2002-217020/27
                                                                                                                                                                                                                                                                                                                                                                                                     20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL88549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200207678-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olivera BM,
Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2002
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      Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB88283;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COGN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeninal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducting neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
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New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.3%; Score 133; DB 23; Length 75; 95.0%; Pred. No. 1.2e-07; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative disease; neuromuscular disorder.
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Misc-difference 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Trp, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB88284 standard; Peptide; 20 AA.
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                                                                                                                                                                        Claim 9; Page 56; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C striatus mu-conopeptide S3-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-245157P.
2001US-264319P.
2001US-277270P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-2001; 2001WO-US23125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 95.0 nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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29-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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amyotrophic lateral sclenosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-horpetic neuralgia, neuromuscular diabetic neuropathy, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystomia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                      The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as
                                                                                                                                        New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
            Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anaesthetic, neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antidajing; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
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         Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.3%; Score 117; DB 23; Length 20; 94.7%; Pred. No. 2.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
      Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C stercusmuscarum mu-conopeptide SEQ ID NO: 473.
                                  Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
   Garrett JE,
                            Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                Claim 1; Page 56; 231pp; English.
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   Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2002 (first entry)
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                                                                                                                                                                                                                                       neuroprotective agents
                                  Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus stercusmuscarum
                                                                                  WPI; 2002-217020/27.
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Best Local Similarity
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Olivera BM,
                               Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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ABB88344 standard; Protein; 76 AA
                                            Claim 1; Page 83; 231pp; English.
                                                                                                                                                                                                                 1 ZNCCNG--GCSSKWCRDHARCC 20
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2001US-264319P.
2001US-277270P.
                                                                                                                                                                                          77.38;
                                                                                                                                                                                    82.8%;
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                                                                                                                                                                                                  17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-217020/27.
                                                                                                                                                                                           Local Similarity
                                                                                                                                                                    22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABL88578.
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                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                   ABB88344;
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                             ABB88344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garrett JE, Watkir
rtier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-2000; 2000US-219619P.
03-NOV-2000; 2000US-245157P.
29-JAN-2001; 2001US-264319P.
21-MAR-2001; 2001US-277270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-2001; 2001WO-US23125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COGN-) COGNETIX INC
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Olivera BM, Jacobsen R,

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amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, obst-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
                                                                                                                                                                                                                                                                                                    The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as
New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 111; DB 23; Length 22; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C stercusmuscarum mu-conopeptide Sm3-3 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M, Garrett JE, Watki
Cartier GE, Shen GS;
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in channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neurodegenerative disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuromuscular disorders, burn pain, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, rischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, troating essential infarct, physical trauma, providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                           The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
blocking agents, as local anesthetic agents, as analgesic agents and as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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                                                                                                                                                                                                                                                                                                                                                                           Score 110; DB 23; Length 76;
Pred. No. 3.6e-05;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurodegenerative disease; neuromuscular disorder.
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rtier GE, Shen GS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "OTHER=pyroGlu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Trp, OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                            Claim 9; Page 69; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB88345 standard; Peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ZNCCNG--GCSSKWCRDHARCC 20
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2000US-245157P.
2001US-264319P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-2001; 2001WO-US23125
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                                                                                                                                                                                                                                                                                                                                                                                        82.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 72.7
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus stercusmuscarum
                            neuroprotective agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 14
                                                                                                                                                                                                                                                                                                                                                      76 AA;
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03-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                          Sequence
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ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herptetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotaxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, crowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence
                                                                                                                                                 The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated
                         New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shon K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 70.1%; Score 94; DB 23; Length 22; 75.0%; Pred. No. 0.00071; ...,ve. 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garrett JE, Watkins M,
rtier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C consors mu-conopeptide SEQ ID NO: 474.
                                                                                                                                                                                                                                                                                                                                                                is a mu-conopeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB88491 standard; Peptide; 22 AA.
                                                                                                                        Claim 1; Page 69; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-245157P.
2001US-264319P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CCNG--GCSSKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-219619P.
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Jacobsen R, Jones RM, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 75.0 nes 15; Conservative
                                                                                        neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COGN-) COGNETIX INC
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WPI; 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                                                         22 AA;
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03-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phytai, or hypodyycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents
blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective, anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
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                                                                                                                                                                                                                                                                                                                                                           63.4%; Score 85; DB 23; Length 22; 60.0%; Pred. No. 0.0067;
                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garrett JE, Watki
rtier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C consors mu-conopeptide Cn3-3 propeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB88394 standard; Protein; 74 AA.
                                                  Claim 1; Page 83; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-219619P.
2000US-245157P.
2001US-264319P.
2001US-277270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                3 CCN--GGCSSKWCRDHARCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones RM,
                  neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             22 AA;
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated in channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuroamuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroamal pain and phantom limb, burn pain, post-herpetic neuralgia, neuroamal pain and phantom limb, burn pain, or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as physia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shon K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.4%; Score 85; DB 23; Length 74; 60.0%; Pred. No. 0.018;
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Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Claim 9; Page 80; 231pp; English.
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21-MAR-2001; 2001US-277270P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COGNETIX INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AA;
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amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypodyvacemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
ion channels. These may include neurodegenerative disorders such as
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Seguence

62.7%; Score 84; DB 23; Length 26; 56.0%; Pred. No. 0.0099; 2; Indels 3; Mismatches 1 ZNCCN----GGCSSKWCRDHARCC 20 3 DRCCNKGNGKRGC-SRWCRDHSRCC 26 Conservative Local Similarity es 14; Conserv Query Match Matches g ó

Gaps

ABB88167 standard; Protein; 80 ABB88167; RESULT 10 ABB88167

bullatus mu-conopeptide Bu3-3 propeptide. (first entry) 24 - MAY - 2002

Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.

Conus bullatus

31-JAN-2002

23-JUL-2001; 2001WO-US23125.

21-JUL-2000; 2000US-219619P. 03-NOV-2000; 2000US-245157P. 29-JAN-2001; 2001US-264319P.

21-MAR-2001; 2001US-277270P.

(UTAH) UNIV UTAH RES FOUND.

COGN-) COGNETIX INC.

Shon K; Watkins M, Cruz LJ, Shen GS; Garrett JE, Cartier GE, Mcintosh JM, Jones RM, WPI; 2002-217020/27. N-PSDB; ABL88496 Olivera BM, Jacobsen R,

New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as

Claim 9; Page 29; 231pp; English.

neuroprotective agents

The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,

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post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; artidiabetic; cardiavascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
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Cartier GE, Shen GS;
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                              62.7%; Score 84; DB 23; Length 80; 56.0%; Pred. No. 0.024;
                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                     3; Mismatches
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                                                                                                                                                                                                                                                                                              1 ZNCCN----GGCSSKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                    ABB88510 standard; Peptide; 23 AA.
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03-NOV-2000; 2000US-245157P.
29-JAN-2001; 2001US-264319P.
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Matches 14; Conserv
                                                                                                                                                                            80 AA;
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New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                 3,
                                                                                                                                                                            Score 83.5; DB 23; Length 23; Pred. No. 0.01; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C bullatus mu-conopeptide Bu3-1A propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 28; 231pp; English.
                                                                                                                                                                                                                                                                                                                    3 DRCCKGKRGC-GRWCRDHSRCC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB88163 standard; Protein; 77
                                                                                                                                                                                                                                                                                      1 ZNCCNG--GCSSKWCRDHARCC 20
                                                                                                                                                                                    62.3%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-245157P.
2001US-264319P.
2001US-277270P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcintosh JM,
                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-217020/27.
                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABL88494
                                                                                                                                       23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200207678-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus bullatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 - MAY - 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JAN-2002
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB88163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olivera
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, brain or spinal cord trauma, myocardial infarct, physical accident, brain or spinal cord trauma, myocardial infarct, physical trauma, providing muscle relaxation, treating essential bloppharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                              Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shon K;
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                             anaesthetic, neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cruz LJ,
                                                            Length 77;
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watkins M,
                                                              Score 83.5; DB 23;
is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M, Garrett JE, Watki
Cartier GE, Shen GS;
                                                                             Pred. No. 0.027;
                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                 C bullatus mu-conopeptide SEQ ID NO: 494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 84; 231pp; English.
                                                                                                                                                                                                                                        ABB88511 standard; Peptide; 24 AA
                                                                                                                            20
                                                                                                                                                        74
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2000US-245157P.
2001US-264319P.
2001US-277270P.
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                                                              62.3%;
59.1%;
                                                                                                                             1 ZNCCNG--GCSSKWCRDHARCC
                                                                                                                                              54 DRCCKGKRGC-GRWCRDHSRCC
                                                                                                                                                                                                                                                                                                      24-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcintosh JM,
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-217020/27.
                                                               Query Match
Best Local Similarity
                                 77 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus bullatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200207678-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olivera BM,
                                                                                               13;
                                   Sequence
                                                                                                 Matches
                                                                                                                                                                                                          RESULT 13
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                                                                                                                                 ò
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24 AA;

Sequence

The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, accident, as unforcation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence

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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated but channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as physia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystohia, and for anti-winkle use. The present sequence is a mu-conopeptide preprotein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mu-conopeptides useful for treating disorders associated with
                                                                         4;
61.2%; Score 82; DB 23; Length 24; 60.9%; Pred. No. 0.015;
                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4, Garrett JE, Watkir
Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C bullatus mu-conopeptide Bu3-2 propeptide.
                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   ABB88165 standard; Protein; 78 AA.
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                                                                                                                                  1 ZNCC-NG--GCSSKWCRDHARCC 20
                                                                                                                                                                     : || || || :|||||| 3 ERCCKNGKRGC-GRWCRDHSRCC 24
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29-JAN-2001; 2001US-264319P.
21-MAR-2001; 2001US-277270P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                            Best Local Similarity 60.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcintosh JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-217020,
N-PSDB; ABL88495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 - MAY - 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB88165;
Query Match
                                                                                                                                                                                                                                                                                                    RESULT 14
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amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotaxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, abrain or spinal cond trauma, myocardial infarct, physical trauma, and the stroke is the stroke of the stroke or is the stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective, anticonvulsant; antiaging; antidiabetic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular diseards.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75.5; DB 23; Length 23;
Pred. No. 0.074;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcintosh JM, Garrett JE, Watkir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C bullatus mu-conopeptide SEQ ID NO: 492.
                                                                                                                                                                                                                                                                                                                           ABB88509 standard; Peptide; 23 AA
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    20
                                                         54 ERCCKNGKRGC-GRWCRDHSRCC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
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1 ZNCC-NG--GCSSKWCRDHARCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.3%;
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2001US-264319P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2002 (first entry)
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Best Local Similarity
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03-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                      ABB88509;
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7

Gaps

4;

2; Indels

61.2%; Score 82; DB 23; Length 78; 60.9%; Pred. No. 0.039;

Pred. No. 0.039; ; Mismatches

3;

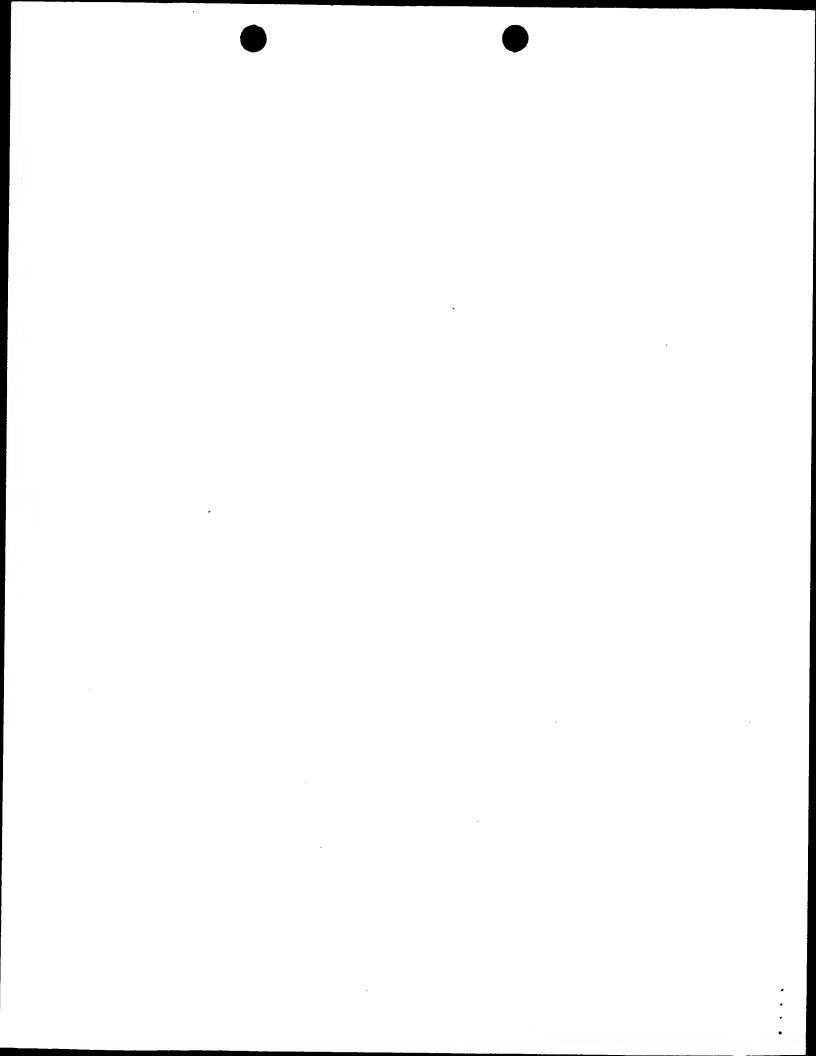
14; Conservative

Matches

Best Local Similarity

Query Match

Search completed: January 10, 2003, 08:35:36 Job time : 27.5942 secs



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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

January 10, 2003, 08:32:32; Search time 6.43478 Seconds (without alignments) 298.796 Million cell updates/sec Run on:

Title: Perfect score:

US-09-910-009A-432 134 1 ZNCCNGGCSSKWCRDHARCC 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dЮ			COLUMNIC	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	54	40.3	362	2	T52038	probable phytochel
7	53.5	39.9		7	F72616	hypothetical prote
e	53	39.6	223	7	B38346	ultra-high-sulfur
4	53	39.6		7	A38346	ultra-high-sulfur
S	52	38.8		-	S18946	ultra high-sulfur
9	51.5	38.4		7	A34484	metallothionein I
7	51.5	38.4	2910	7	T42214	otogelin - mouse
80	S	38.1		7	н86231	hypothetical prote
σ	50.5	37.7		7	148141	acrogranin - quine
10	20	37.3		7	T46722	hyr
11	20	37.3		٦	KHRZOB	oryzain (EC 3.4.22
12	20	37.3	11	7	S40241	G protein-coupled
13		36.2		C¥	S47576	metallothionein 20
14		36.2		7	S39420	metallothionein 20
15	48.5	36.2		7	S39421	metallothionein 20
16		36.2		7	T49670	hypothetical prote
17		36.2		7	T18975	
18	•	36.2		7	T24272	
19	48.5	36.2	4	7	E96745	
20		36.2		~	T01206	cysteine proteinas
21	48	35.8		7	G87164	hypothetical prote
22	48	35.8		Н	DWDXAF	2-hydroxyglutaryl-
23	48	35.8		7	A38314	L-amino-acid oxida
24	48	35.8		7	T00266	hypothetical prote
25	47.5	35.4		~	JC6547	high sulfur protei
56		35.4		7	T00480	RI
27	47.5	35.4	1172	7	F84572	probable cadmium-t
28	47	35.1		CI	$\overline{}$	antileukoproteinas
29	47	35.1		7	F96566	F6D8.19 [imported]

hypothetical prote	hypothetical prote	probable phytochel	cysteine proteinas	hypothetical prote	neuronal apoptosis	granulin precursor	metallothionein 1	hypothetical prote	Beta-microseminopr	epididymis-specifi	hypothetical prote	cysteine proteinas	late competence pr	cysteine proteinas	transponson protei
T15651	B84637	T51392	S24602	T47184	A55478	GYHU	A34905	T24715	A59385	S25454	C97102	JA0159	B30338	T06416	T31197
~	7	7	7	7	~	П	7	7	7	7	~	7	~	7	2
188	198	395	464	206	1232	593	63	74	90	125	299	346	356	466	710
35.1	35.1	35.1	35.1	35.1	35.1	34.7	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3
7 1	7.7	47	47	47	47	46.5	46	46	46	46	46	46	46	46	46
4.															

ALIGNMENTS

Gaps ; Indels . 9 Pred. No. 22; 2; Mismatches 50.0%; Conservative Best Local Similarity Matches 8; Conserv Matches

ó

NCCNGGCSSKWCRDHA 17 7 QΫ qq

RESULT 2

hypothetical protein APE1391 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
A;Species: A; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-no, K.
Awarabayasi, Y; Hino, Y; Horikawa, H; Yamazaki, S; Haikamiya, M; Masuda, S; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <KAM>A;Cross-references: DDBJ:AP000061; NID:95104821; PIDN:BAA80388.1; PID:95105074
A;Experimental source: strain K1
C;Genetics:

A;Gene: APE1391 C;Superfamily: Aeropyrum pernix hypothetical protein APE1391

Gaps ŝ Length 258; Indels DB 2; Ouery Match 39.9%; Score 53.5; Di Best Local Similarity 47.1%; Pred. No. 20; Matches 8; Conservative 1; Mismatches

1;

4 CNGGCSSKWCRDHARCC 20 Οy

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metallothionein I - yeast (Candida glabrata)

C;Species: Candida glabrata
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C;Accession: A34484
E;Mehrat, R.K.; Garey, J.R.; Butt, T.R.; Gray, W.R.; Winge, D.R.
J. Biol. Chem. 264, 1947-19753, 1989
A;Title: Candida glabrata metallothioneins. Cloning and sequence of the genes and cha A;Reference number: A92737; MUID:90062075; PMID:2584191
A;Accession: A34484
A;Molecule type: DNA
A;Residues: 1-63 <MEH>
                                                                                                                                                                                     A.Cross-references: EMBL:X63755; NID:932471; PIDN:CAA45283.1; PID:932472
R;MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.
J. Cell Biol, 111, 2587-2600, 1990
A;Title: Structure and expression of genes for a class of cysteine-rich proteins of A;Reference number: A36686; WUID:91115951; PMID:1703541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:J05133; NID:g173321; PIDN:AAA35272.1; PID:g173322 A;Note: the authors translated the codon GAG for residue 61 as Asp C;Superfamily: metallothionein
submitted to the EMBL Data Library, December 1991
A;Description: Nucleotide sequence of a Human high-sulphur Keratin cDNA.
A;Reference number: S18946
                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-39,'Y',41-169 <MAC>
A;Cross-references: GB:X55293; NID:934078; PIDN:CAA39005.1; PID:934079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        otogelin - mouse
N;Alternate names: mucin-like extracellular matrix protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.8%; Score 52; DB 1;
44.4%; Pred. No. 23;
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51.5; DE Pred. No. 14; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,map position: IIq13-11q13
C; Superfamily: ultra-high-sulfur keratin
C; Keywords: hair; tandam repeat
F; 7-19/Region: Ser-rich nonapeptide repeat
F; 59-68/Region: Gly-rich decapeptide repeat
F; 69-78/Region: Gly-rich decapeptide repeat
F; 79-78/Region: Cys-rich decapeptide repeat
F; 89-97/Region: Cys-rich decapeptide repeat
F; 98-107/Region: Cys-rich decapeptide repeat
F; 108-117/Region: Cys-rich decapeptide repeat
F; 118-126/Region: Cys-rich decapeptide repeat
F; 127-136/Region: Cys-rich decapeptide repeat
F; 117-145/Region: Cys-rich decapeptide repeat
F; 16-155/Region: Cys-rich decapeptide repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GDB:125257; OMIM:148021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.4%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CCNGGCSSKWCRDHARCC 20
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 8; Conserv
                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-169 <DRA>
                                                                                                            A; Accession: S18946
                                                                                                                                                                                                                                                                                                                                                        A;Accession: B36686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: KRN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T42214
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C;Species: Mus musculus (house mouse)
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
C;Accession: A38346
E;Mood, L; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin expression: A38346; MUID:91065960; PMID:2250030
A;Reference number: A38346; MUID:91065960; PMID:2250030
                                                                                                                                                                  ultra-high-sulfur keratin 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C;Accession: A38660; B38346
E;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 266, 4024, 1991
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin (A;Reference number: A38660; MUID:91154184; PMID:1840598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-21,'GGCGSGCGGCGSNCGGCGSSCCKPVCC',22-40,'GSS',44-45,'G',47-48,'S',50,'GSS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 265, 21375-21380, 1990.
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A;Reference number: A38346; MUID:91065960; PMID:2250030
A;Accession: B38346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
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$18946
ultra high-sulfur keratin 1 - human
ultra high-sulfur keratin; ultra high-sulfur matrix protein
N;Alternate names: UHS keratin; ultra high-sulfur matrix protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Oct-1999 #sequence_revision 22-Oct-1999
C;Accession: S18946; B3666
R;Drabent, B.; Doenecke, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962 A;Note: the sequence reported in this paper has been corrected. See A38660 C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-23 <MOS-
A; Cross-references: GB:M37760; NID:9200963; PIDN:AAA40107.1; PID:9200964
A; Note: this is a correction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 2; Length 223;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ultra-high-sulfur keratin 1 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 CCSSGCGSSCCQ--SSCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 ccsscccsscco--sscc 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CCNGGCSSKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CCNGGCSSKWCRDHARCC 20
                   231 CLGGCRGRWC----CC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 8: Conserv
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A; Residues: 1-230 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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                                                                                                            RESULT 3
B38346
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Gaps

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Indels

Length 169;

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Gaps

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6; Indels

Length 63;

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A;Cross-references: GB:M86735; NID:g191234; PIDN:AAA37030.1; PID:g191235
C;Superfamily: granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Experimental source: strain Friedlin C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.38;
                                                                                              37.78;
33.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 40.9
nes 9; Conservative
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                                                                                                                                                        Conservative
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A; Residues: 1-471 <WAT2>
                                                                                                                     Local Similarity
nes 10; Conserv
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Lin, Y.; Lin, X.; Liu, Z.X.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Baba, T.; Hoff, H.B.
Mol. Reprod. Dev. 34, 233-243, 1993
A;Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor of the grd
A;Reference number: 148141; MUID:93228994; PMID:8471244
                                                                                           R;Cohen-Salmon, M.; El-Amraoui, A.; Leibovici, M.; Petit, C.
Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997
Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997
A;Title: Otogelin: A glycoprotein specific to the acellular membranes of the inner ear.
A;Reference number: 222079; MUID:98070772; PMID:9405633
A;Accession: T42214
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Gecule type: mRNA
A;Residues: 1-2910 «COH>
A;Residues: 1-2910 «COH>
A;Residues: Embil 96411; NID:92760883; PID:92760884; PIDN:AAB96561.1
A;Cross-references: EMBL:U96411; NID:92760883; PID:92760884; PIDN:AAB96561.1
A;Rote: component of all the acellular membranes of the inner ear
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
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A;Residues: 1-454 <STO>
A;Cross-references: GB:AE005172; NID:g2160169; PIDN:AAB60732.1; GSPDB:GN00141
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C;Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                    C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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0
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42.9%; Pred. No. 1.6e+02;
tive 4; Mismatches 5; Indels 3.
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57;
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A;Molecule type: mRNA
A;Residues: 1-591 <RES>
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 CQSGGDEATWCRALMEYARAC 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.1%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 42.99
Matches 9; Conservative
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Matches 8; Conserv
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                                                                                   C; Accession: T42214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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A; Molecule type: mRNA
A; Residues: 1-471 < MAT1>
R; Watanabe, H.; Abe, K.; Emori, Y.; Hosoyama, H.; Arai, S.
B; Watanabe, H.; Abe, K.; Emori, P.; Hosoyama, H.; Arai, S.
Biol. Chem. 266, 16897-16902, 1991
A; Title: Molecular cloning and gibberellin-induced expression of multiple cysteine pr A; Reference number: A40053; MUID:91358494; PMID:1885617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.G.
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R;Volckaert, G.; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, Submitted to the EMBL Data Library, December 1999
A;Reference number: Z23137
A;Accession: T46722
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                            5;
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C, Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: probable proline synthetase associated protein
C;Species: Leishmania major
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
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                                                                Gaps
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C;Superfamily: papain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;361-471/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;161-204,195-237,295-346/Disulfide bonds: #status predicted F;164,301,321/Active site: Cys, His, Asn #status predicted F;340,388/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.3%; Score 50; DB 1; Length 471; 40.9%; Pred. No. 76; tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                Indels
                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein (imported) - Leishmania major
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R;Watanabe, H.; Abe, K.; Emori, Y.; Hosoyama, H.; Arai, S.
submitted to JIPID, May 1991
A;Reference number: JU0388
A;Accession: JU0389
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      2;
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67;
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      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                1; Mismatches
Score 50.5; Pred. No. 77;
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                                                                                                                                                                                      293 QTCCRLQ-SGKWGCCPFPKAVCCEDHVHCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50;
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                                                                                                                            1 ZNCCNGGCSSKW-----CRDHARCC 20
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5 NCIETNVCICGTGCSGKCCRCGDACKC 31
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C;Superfamily: metallothionein
C;Keywords: chelation; metal binding
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A,Residues: 1-71 AMAC>
C,Superfamily: metallohionein
C,Keywords: chelation; metal binding
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: precliminary
A.Status: 1-115 cTERN
A.Cross-references: EMBL:223104; NID:9438128; PID:9438129
C.Superfamily: great pond snail LDL receptor-related G protein-coupled receptor; transmembrane protein
C.Keywords: G protein-coupled receptor; transmembrane protein
F;38-77/Domain: LDL receptor ligand-binding repeat homology <LDLL>
F;18-134/Domain: LDL receptor ligand-binding repeat homology <LDLL>
F;18-134/Domain: LDL receptor ligand-binding repeat homology <LDLL>
F;23-257/Domain: LDL receptor ligand-binding repeat homology <LDLL>
F;23-257/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;23-257/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;327-361/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;367-401/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;466-440/Domain: LDL receptor ligand-binding repeat homology <LDRC>
F;466-440/Domain: LDLC receptor ligand-binding repeat homology <LDRC>
F;466-440/Domain: LDLC receptor ligand-binding repeat homology <LD
                                                                                                                                                                                                                                                                                                                                                                                                    C, Accession: S40241
R; Tensen, C.P.; Kesteren, E.R.; Planta, R.J.; Cox, K.; Burke, J.F.; Heerikhuizen, H.; Vr submitted to the EMBL Data Library, June 1993
A; Description: A G protein-coupled receptor with LDL-binding motifs suggests a role for A; Reference number: S40241
A; Accession: S40241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Mytilus edulis (Diue mussel)
C; Species: Mytilus edulis (Diue mussel)
C; Species: Mytilus edulis (Diue mussel)
C; Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 17-Mar-1999
C; Accession: S4756
Eur. J. Biochem. 218, 183-194, 1993
A; Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal A; Reference number: S39416; MUID: 94062828; PMID: 8243463
A; Mccession: S47576
A; Molecule type: protein
A; Molecule type: protein
A; Mesidues: 1-71 kMAC;
C; Superfamily: metallothionein
C; Superfamily: metallothionein
C; Keywords: chelation; metal binding
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                                                                                                                                                                                                                                                                                      G protein-coupled receptor - great pond snail
C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDL receptor ligand-binding repeat homology CLDL8>
leucine-rich alpha-2-glycoprotein repeat homology CLRR1>
leucine-rich alpha-2-glycoprotein repeat homology CLRR2>
leucine-rich alpha-2-glycoprotein repeat homology CLRR2>
leucine-rich alpha-2-glycoprotein repeat homology CLRR3>
leucine-rich alpha-2-glycoprotein repeat homology CLRR4>
leucine-rich alpha-2-glycoprotein repeat homology CLRR4>
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Pred. No. 1.3e+02;
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40.7%; Pred. No. 33;
Live 1; Mismatches
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                                                                     407 CLVWGCCPVEGATCCKDHASCC 428
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                        3 CCNGGC----SSKWCRDHARCC 20
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Matches 11; Conserve
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F; 656-679/Domain:
F; 704-727/Domain:
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Rimackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R. Eur. J. Blochem. 218, 183-194, 1993
A;Title: Complete amino acid sequences of five dimeric and four monomeric forms of me A;Reference number: 839416; MUID:94062828; PMID:8243463
A;Reference number: S39420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S39421
R; Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R. Eur. J. Blochem. 218, 183-194, 1993
A; Title: Complete amino acid sequences of five dimeric and four monomeric forms of me A; Reference number: S39416; MUID:94062828; PMID:8243463
metallothionein 20-Ia - blue mussel
C:Species: Mytilus edulis (blue mussel)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
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C;Species: Mytilus edulis (blue mussel)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
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Gaps

7

Gaps

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GenCore version 5.1.3
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OM protein - protein search, using sw model

January 10, 2003, 08:32:27 ; Search time 98.4783 Seconds Run on:

(without alignments)
101.482 Million cell updates/sec

US-09-910-009A-210 Perfect score:

1 GSMMSKLGVLLTVCLLLFPL.....CCNGGCSSKWCRDHARCCGR 75 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDS2/gcgdata/geneseqp-emb1/AA1982.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Caco-ma min-copo	O Ottoriomonia	C a cer cualitascat mil	C consors mi-conon	Chullatus miscoop	כ מתדדמרים ווות כסווס	C CODSOLS MI-CODOD	Chillatus mitodo	Contracts ma como	C tulipa mu-conope	Commissione D	ממדמדמדמד ווומ	C nobilis mu-conop	J	c cultpa mu-conope
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37	33	ABB88277	ABB88161	ABB88238	ABB88236	332	\sim		~	~	17	ABB88205	~	ABB88279		ABB88326		319	ABB88342	324	ABB88242	327	ABB88228	ABB88153	ABB88171	ABB88218	ABB88263	ABB88271	4	σ	BB8	322	BB8824	BB8817
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ALIGNMENTS

ABB88283

ABB88283 standard; Protein; 75 AA

ABB88283;

(first entry) 24 - MAY - 2002

C striatus mu-conopeptide S3-2 propeptide.

Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antidajng; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.

Conus striatus.

WO200207678-A2.

31-JAN-2002

23-JUL-2001; 2001WO-US23125

03-NOV-2000; 2000US-245157P. 29-JAN-2001; 2001US-264319P. 21-MAR-2001; 2001US-277270P. 2000US-219619P 21-JUL-2000;

(UTAH) UNIV UTAH RES FOUND.

Mcintosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K; Olivera BM,

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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegeneative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, or ischaemia which typicall pain and sasociated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, trowning, suffocation, perinatal as physia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                     voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GSMMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anaesthetic; neuromusular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                    New mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 420; DB 23; Length 75; 100.0%; Pred. No. 1.4e-40; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stercusmuscarum mu-conopeptide Sm3-3 propeptide.
Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
 Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB88344 standard; Protein; 76 AA.
                                                                                                                                                                               Claim 9; Page 56; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-245157P.
2001US-264319P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-219619P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2001; 2001WO-US23125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.4
Best Local Similarity 100.4
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CSSKWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSSKWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus stercusmuscarum.
 Jacobsen R, Jones RM,
                                                                                                                                                neuroprotective agents
                                       WPI: 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200207678-A2.
                                                          N-PSDB; ABL88549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 - MAY - 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB88344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB88344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                               New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNG--G 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Shon K;
   Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 372; DB 23; Length 76;
Pred. No. 4.4e-35;
5; Mismatches 2; Indels
 M, Garrett JE, Watkins M,
Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C consors mu-conopeptide Cn3-3 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB88394 standard; Protein; 74 AA.
                                                                                                                                                                                          Claim 9; Page 69; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
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03-NOV-2000; 2000US-245157P.
29-JAN-2001; 2001US-264319P.
21-MAR-2001; 2001US-277270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2001; 2001WO-US23125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.6%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 88.0
nes 66; Conservative
       Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSSKWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSSRWCRDHSRCCGR 75
                                                                                                                                                          neuroprotective agents
                      Jones RM,
                                                        WPI; 2002-217020/27
N-PSDB; ABL88578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200207678-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2002
        Olivera BM,
                          Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB88394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders with as amyotrophic lateral sclerosis, neuroamuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroamuscular and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cond trauma, myocardial infarct, physical trauma,
                                                                                                                                                                                                                                                                                                                                                                      drowning, suffocation, perinatal as phyxia, or hypodycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence
                                                                                                                blocking agents, as local anesthetic agents, as analyesic agents and as neuroprotective agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                 Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCN--GG 60
                                                                                                           mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
               Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
               Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 335; DB 23;
Pred. No. 7.3e-31;
6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                           is a mu-conopeptide preprotein of the invention
             M, Garrett JE, Watkin
Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bullatus mu-conopeptide Bu3-3 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB88167 standard; Protein; 80 AA
                                                                                                                                                                                           Claim 9; Page 80; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-219619P.
2000US-245157P.
2001US-264319P.
2001US-277270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.8%;
79.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-2001; 2001WO-US23125.
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               Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CSSKWCRDHARCCG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CSGRWCRDHAQCCG 74
                                                             WPI; 2002-217020/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 AA;
                                                                            N-PSDB; ABL88603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200207678-A2
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29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 - MAY - 2002
                            Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                     ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cond trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                                                                          present invention relates to mu-conopeptides derived from snails, the can be in the treatment of disorders associated with voltage-gated
                                                                                                                                               voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                   Cruz LJ, Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKR--QNCCN-- 58
                                                                                                                              mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                   Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 320; DB 23;
Pred. No. 4.1e-29;
                                                Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C consors mu-conopeptide Cn3-4 propeptide.
                                   Garrett JE,
                                                Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB88396 standard; Protein; 76 AA.
                                                                                                                                                                                                            Claim 9; Page 29; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-245157P.
2001US-264319P.
2001US-277270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- GGCSSKWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001; 2001WO-US23125
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                                Olivera BM, Mcintosh JM,
Jacobsen R, Jones RM, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                            neuroprotective agents
(COGN-) COGNETIX INC
                                                                             WPI; 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 AA;
                                                                                              N-PSDB; ABL88496
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29-JAN-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Sim.
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                               which
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ABB88396
   οy
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Ξ,
                                                                                                                                                                                                                                                             The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, post-herpetic neuropial, injury associated with hypoxia, anoxia or ischaemia which trgically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, brownigh suffocation, perinatal as physia, or hypodytocamic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                                                              New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                               Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCC---NG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 306.5; DB 23; Length 76; Pred. No. 1.3e-27;
                                               Watkins M, Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative disease; neuromuscular disorder,
                                               (, Garrett JE, Watki)
Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C bullatus mu-conopeptide Bu3-2 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB88165 standard; Protein; 78 AA.
                                                                                                                                                                                                                                      Claim 9; Page 80; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-219619P.
2000US-245157P.
2001US-264319P.
2001US-277270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.0%;
76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-2001; 2001WO-US23125
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                 Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 76.3
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 GCSSKWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SCSGKACKSLKCCSGR 76
                                                                 Jones RM,
                                                                                                                                                                                                        neuroprotective agents
                 (COGN-) COGNETIX INC.
                                                                                                2002-217020/27.
                                                                                                                  N-PSDB; ABL88604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-NOV-2000;
29-JAN-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 - MAY - 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002.
                                                  Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB88165;
                                                                    Jacobsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB88165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                     as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                      Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKR--QNCC-NG 59
                                                                                                                                                  New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective, anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
9
                                                        Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                          Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 306; DB 23;
Pred. No. 1.6e-27;
                                                                       Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C tulipa mu-conopeptide T3-2 propeptide.
                                                          4, Garrett JE,
Cartier GE, Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB88318 standard; Protein; 75 AA.
                                                                                                                                                                                                                                     Claim 9; Page 29; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-219619P.
2000US-245157P.
2001US-264319P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.9%;
75.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUL-2001; 2001WO-US23125.
           (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRGC-GRWCRDHSRCCGR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GCSSKWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                           JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                       neuroprotective agents
                                                                            Jones RM,
                                                          BM, Mcintosh
                               (COGN-) COGNETIX INC
                                                                                                        WPI: 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 AA;
                                                                                                                       N-PSDB; ABL88495
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29-JAN-2001;
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                                                                          Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB88318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                           Olivera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus
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                                                                                                                                                                                                       The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, to providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                                                                    as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                         Shon K;
                                                                                                                                       voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNG--G 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                            New mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; Length 75;
                                                         Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                         Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                             72.5%; Score 304.5; DB 23; 74.7%; Pred. No. 2.3e-27; ive 9; Mismatches 7;
                                               Garrett JE, Waln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C aurisiacus mu-conopeptide A3-3 propeptide.
                                                                     Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB88149 standard; Protein; 78 AA
                                                                                                                                                                                     Claim 9; Page 64; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-2000; 2000US-219619P. 03-NOV-2000; 2000US-245157P.
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 21-MAR-2001; 2001US-277270P.
                        (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                           Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CSSKWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CSSRECRPQ-HCCGR 74
                                                                                                                                                             neuroprotective agents
                                                                     Jones RM,
                                                          Mcintosh
                                   (COGN-) COGNETIX INC
                                                                                           WPI; 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                           75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus aurisiacus.
                                                                                                      N-PSDB; ABL88566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200207678-A2.
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                                                           Olivera BM,
                                                                    Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB88149;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystohia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                                                                                                                                                                                             New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents
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                                                                                                                                                                                     Watkins M, Cruz LJ, Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GSMMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCC--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.3%; Score 303.5; DB 23; Length 78; 71.8%; Pred. No. 3.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pred. No. 3.1e-27;
); Mismatches 10
                                                                                                                                                                                     4, Garrett JE, Watkin
Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C nobilis mu-conopeptide Nb3-2 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB88261 standard; Protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 25; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
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                           21-MAR-2001; 2001US-277270P.
29-JAN-2001; 2001US-264319P.
                                                                                                (UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KGSCSGKACKNLKCCSGR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2002 (first entry)
                                                                                                                                                                                            Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                              Jones RM,
                                                                                                                              (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                         WPI; 2002-217020/27
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                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL88487
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                                                                                                                                                                                            Olivera BM,
                                                                                                                                                                                                                              Jacobsen R,
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuroamscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroamal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischmenia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, browning, suffocation, perinatal as physia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystomia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                                                                        New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                               Garrett JE, Watkins M, Cruz LJ, Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GSMMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCC--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antidaing; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.3%; Score 303.5; DB 23; Length 78; 71.8%; Pred. No. 3.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C tulipa mu-conopeptide T3-1 propeptide.
                                                                                                                                                  Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB88299 standard; Protein; 74 AA,
                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 51; 231pp; English.
03-NOV-2000; 2000US-245157P.
29-JAN-2001; 2001US-264319P.
21-MAR-2001; 2001US-277270P.
                                                                        (UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                 Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarics
".+rhes 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 NGGCSSKWCRDHARCCGR
                                                                                                                                                                                                                                                                                               neuroprotective agents
                                                                                                                                                  Jones RM,
                                                                                                                                                                                      WPI; 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 AA;
                                                                                                                                                                                                     N-PSDB; ABL88539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200207678-A2.
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                                                                                                                               Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2002.
                                                                                                                                                Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated and channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neurolgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, myocardial infarct, physical trauma, perinatal as phyta, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 7
                                                                                                                                                                                                                                                       voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                       Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNG--GC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anaesthétic; neuromuscular blocking agént; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                           New mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        χ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.3%; Score 299.5; DB 23; Length 74; 74.3%; Pred. No. 8.3e-27; Indels 3;
                                                                                                                                         Cruz LJ,
                                                                                                                                         Watkins M,
                                                                                                                         Garrett JE, Walna...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bullatus mu-conopeptide Bu3-1A propeptide.
                                                                                                                                                       Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB88163 standard; Protein; 77 AA.
                                                                                                                                                                                                                                                                                                                         Claim 9; Page 60; 231pp; English.
                2000US-245157P.
2001US-264319P.
 2000US-219619P.
                                                 21-MAR-2001; 2001US-277270P.
                                                                                   (UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
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                                                                                                                                       Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 74.3
nes 55; Conservative
                                                                                                                                                                                                                                                                                           neuroprotective agents
                                                                                                                                                         Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSKWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SSRECRPQ-HCCGR 73
                                                                                                                                                                                       2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 AA;
                                                                                                                                                                                                         N-PSDB; ABL88557
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21-JUL-2000;
                03-NOV-2000;
29-JAN-2001;
                                                                                                                                       Olivera BM,
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                                                                                                                                                         Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, brain or spinal cord trauma myocardial infarct, physical trauma, perlnatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                                                                                         New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                       Watkins M, Cruz LJ, Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKR--QNCCNG- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anassthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.3%; Score 299.5; DB 23; Length 77; 74.0%; Pred. No. 8.6e-27; live 7; Mismatches 8; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurodegenerative disease; neuromuscular disorder
                                                                                                                                                       Garrett JE, Watki
tier GE, Shen GS;
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                                                                                                                                                                       Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB88320 standard; Protein; 76 AA.
                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 28; 231pp; English.
              2000US-219619P.
2000US-245157P.
2001US-264319P.
                                                                 2001US-277270P
                                                                                                   (UTAH ) UNIV UTAH RES FOUND (COGN-) COGNETIX INC.
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                                                                                                                                                     Mcintosh JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 74.0
nes 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones RM,
                                                                                                                                                                                                      2002-217020/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 AA;
                                                                                                                                                                                                                        N-PSDB; ABL88494
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                                                29-JAN-2001;
                                                                  21-MAR-2001;
                                  03-NOV-2000;
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                                                                                                                                                     Olivera BM,
                                                                                                                                                                       Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, sost-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotakic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrowascular accident, or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as physical or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as
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                                                                                                                                                                    Shon K;
                                                                                                                                                                                                                                                                                    voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                 mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                    Cruz LJ,
                                                                                                                                                                    Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C stercusmuscarum mu-conopeptide Sm3-1 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                  Shen GS;
                                                                                                                                                                    Garrett JE,
                                                                                                                                                                                  Cartier GE,
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                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 64; 231pp; English.
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                                             2000US-245157P.
2001US-264319P.
2001US-277270P.
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71.18;
                               2000US-219619P
23-JUL-2001; 2001WO-US23125.
                                                                                                                (UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                                                                 Olivera BM, Mcintosh JM,
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                                                                                                                                                                                    Jones RM,
                                                                                                                                                                                                                                                                                                                     neuroprotective agents
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                                                                                                                               (COGN-) COGNETIX INC
                                                                                                                                                                                                                WPI; 2002-217020/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 AA;
                                                                                                                                                                                                                                     N-PSDB; ABL88567
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                                                 03-NOV-2000;
29-JAN-2001;
                                                                                21-MAR-2001;
                               21-JUL-2000;
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                                                                                                                                                                                    Jacobsen
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WO200207678-A2
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29-JAN-2001;
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                                                                                    21-JUL-2000;
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31-JAN-2002
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  NAME OF COLOR OF COLO
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                                                                                                                                                                                                                                                                                                                                                                              New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                  Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCC---NGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 292.5; DB 23; Length 75; Pred. No. 5.3e-26; 9; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                     Cruz LJ,
                                                                                                                                                                                                                                                  M, Garrett JE, Watkins M,
Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is a mu-conopeptide preprotein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 54; 231pp; English.
                                                                    21-JUL-2000; 2000US-219619P.
03-NOV-2000; 2000US-245157P.
29-JAN-2001; 2001US-264319P.
21-MAR-2001; 2001US-277270P.
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ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuroduscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord tramma, myocardial infarct, physical tramma, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage gated
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                                                                                                                                                                                                                                                                                                                    Shon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 292.5; DB 23; Length 77; Pred. No. 5.4e-26;
                                                                                                                                                                                                                                                                                                                       Watkins M, Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                     Shen GS;
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                                                                                                                                                                                                                                                                                                                                                         Cartier GE,
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72.78;
                                                                                       03-NOV-2000; 2000US-245157P.
29-JAN-2001; 2001US-264319P.
21-MAR-2001; 2001US-277270P.
23-JUL-2001; 2001WO-US23125.
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es 56; Conserv
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New mu-conopeptides useful for treating disorders associated with voltage gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents.
                                                                                                                               Shon K;
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                                                                                                                              Watkins M,
                                                                                                                            Mcintosh JM, Garrett JE, Watkir
Jones RM, Cartier GE, Shen GS;
                                                                                                                                                                                                                                      Claim 9; Page 46; 231pp; English.
                                              21-JUL-2000; 2000US-219619P.
03-NOV-2000; 2000US-245157P.
29-JAN-2001; 2001US-264319P.
21-MAR-2001; 2001US-277270P.
                             23-JUL-2001; 2001WO-US23125.
                                                                                               (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                         WPI; 2002-217020/27.
N-PSDB; ABL88531.
                                                                                                          (COGN-) COGNETIX INC
         31-JAN-2002.
                                                                                                                            Olivera BM,
Jacobsen R,
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The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischmenta which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, brain or spinal cord trauma, myocardial infarct, physical trauma, providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-winkle use. The present sequence is a mu-conopeptide preprotein of the invention.

3; Gaps 66.1%; Score 277.5; DB 23; Length 74; 71.6%; Pred. No. 2.7e-24; tive 9; Mismatches 9; Indels 3, Conservative Local Similarity hes 53; Conserv 74 AA; Sequence Query Match Best Loca Matches

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3 MMSKLGVLLTVCLLLEPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCN-GGC 61 g

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62 SSKWCRDH--ARCC 73 Q

: ||: || 61 CPVYFRDNFICGCC 74 QQ Search completed: January 10, 2003, 08:35:34 Job time: 98.8116 secs



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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 10, 2003, 08:32:32; Search time 24.1304 Seconds Run on:

(without alignments) 298.796 Million cell updates/sec

US-09-910-009A-210 Title: Perfect score:

1 GSMMSKLGVLLTVCLLLFPL......CCNGGCSSKWCRDHARCCGR 75 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Maximum Match 100% Listing first 45 summaries

Database :

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hromocontropan pr	hynothetical proto	22% antifundal proce	antifungal gosmati		profein H5 - slime	į.	hypothetical prote		anti-mullerian bor	Sensor histidine k	hypothetical prote	unknown protein en		hypothetical prote	CO6G4.1 protein -	DNA-binding protei	G protein-coupled	protein F12K21.20	pristinamycin I sv	2	Cysteine proteinas		acrogranin - diine		hynothetical prote	ς.	hypothetical prote	
SUMMARIES	1D	A58511	ന	JS0646	T02075	A29581	807569	S41614	Н69937	н69711	JC5119	H87561	A90960	B85808	WTBO	T22484	S44748	S61908	S40241	H86468	T30288	D84023	JA0159	T06416	I48141	A42617	T29013		34	8
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59.5	59.5	59.5	59.5	59	59	59	59	59	58.5	58.5	58.5	58.5	58.5	58.5	58.5	
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ALIGNMENTS

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RESULT 1 A58511 bromocontryphan precursor - cone shell (Conus radiatus)

N.Contains: Contryphan; des-Gly-contryphan C.Species: Conus radiatus (radial cone) C.Species: Conus radiatus (radial cone) C.Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 07-May-1999 C.Accession: A58511; B58511; A43097 R.Jimenez, B.C.; Craig, A.G.; Watkins, M.; Hillyard, D.R.; Gray, W.R.; Gulyas, J.; Ri Biochemistry 36, 989-994, 1997 kinshaltional bromination of tryptophan. A:Title: Bromocontryphan: post-translational bromination of tryptophan.

A: Accession: A43097
A: Molecule type: protein
A: Releasation: A43097
A: Molecule type: protein
A: Residues: 55-62 < Unis)
A: Resperimental source: venom
C: Superfamily: unassigned conotoxins
C: Superfamily: unassigned conotoxins
C: Keywords: amidated carboxyl end; bromine: D-amino acid; hydroxyproline; toxin; veno
C: Keywords: amidated carboxyl end; brominental < MAT1>
F: 55-62/Product: contryphan #status experimental < MAT2>
F: 55-62/Product: bromocontryphan #status experimental < MAT2>
F: 55-62/Product: des-Gly-contryphan #status experimental < MAT3>
F: 55-62/Product: des-Gly-contryphan #status experimental < MAT3>
F: 55-62/Product: des-Gly-contryphan #status experimental < MAT3>
F: 55-62/Product: des-Gly-contryphan (Trp) #status experimental
F: 56-Modified site: 6-bromotryptophan (Trp) #status experimental
F: 62/Modified site: amidated carboxyl end (Cys) (amide in mature form from following

6; Mismatches 17; Indels 31; Gaps 17.0%; Score 71.5; DB 2; Length 63; 30.8%; Pred. No. 0.91; 24; Conservative Best Local Similarity Query Match Matches

4 MSKLGVL-LTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCS 62 P

63 SK-----WC qq οy

62

RESULT 2

C83305 hypothetical protein PA2721 [imported] - Pseudomonas aeruginosa (strain PAO1)

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C; Keywords: alpha-amylase inhibitor
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29.8%;
                                                                       16.3%;
29.8%;
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                                                                          Query Match 16.3°
Best Local Similarity 29.8°
Matches 17; Conservative
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A, Molecule type: protein
A, Residues: 1-27 <VIG>
C, Superfamily: thaumatin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A33174
A; Accession: A33174
C; Superfamily: thaumatin I
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Cispecies: Zea mays (maize)
Cibate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 12-Apr-1995
Cibate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 12-Apr-1995
Cibate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 12-Apr-1995
Cibate: 30-Jun-1992 #sequence_revision 130-Jun-1992 #text_change 1300-Jun-1992 #text_change 1300-Jun-1992 #text_change 1300-Jun-1992 #text_change 1200-Jun-1992 #text_cha
                                                                                                                                                                                                                                                                                                   A,Accession: C83305
A;Status: preliminary
A;Status: preliminary
A;Noblecule type: DNA
A;Residues: 1-159 <STO>
A;Cross-references: GB:AE004700; GB:AE004091; NID:g9948792; PIDN:AAC06109.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2721
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83305
R;Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradann, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
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R;Malehorn, D.E.; Borgmeyer, J.R.; Smith, C.E.; Shah, D.M.
Plant Physiol. 106, 1471-1481, 1994
A;Title: Characterization and expression of an antifungal zeamatin-like protein (Zlp) A;Reference number: Z14547; MUID:95148737; PMID:7846159
A;Accession: T02075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 20-Aug-1999
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 20-Aug-1999
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A;Experimental source: strain B73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 KEGDVLIVEFRVMGIPCLGLNGG-PAFRHSEAFSFQVATDDQAETDRIMNALVDNGGEES 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PAERMQDDISSDEHPLFDKRQNCCNGGCSS
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Pred. No. 4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.5%; Score 69.5; DB 2; Best Local Similarity 34.3%; Pred. No. 3.1; Matches 23; Conservative 10; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22K antifungal protein - maize
N;Alternate names: 22K pathogenesis-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antifungal zeamatin-like protein - maize
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29.8%;
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Matches 17; Conservative
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Residues: 1-227 <MAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 ACGWCRD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 K -- WCRD 68
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C; Decies: Dictyostellum discoideum
C; Species: Dictyostellum discoideum
C; Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 23-Mar-2001
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 23-Mar-2001
C; Accession: S0756
B; Singleton, C.K.; Manning, S.S.; Ken, R.
S; Singleton, C.K.; Manning, S.S.; Ken, R.
S; Singleton, C.K.; Manning, S.S.; Ken, R.
S; Mare EmBL Data Library, May 1989
A; Decession: Primary structure and regulation of vegetative specific genes of Dicty
A; Reference number: S07566
A; Accession: S07569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-amylase/trypsin inhibitor - maize alpha-amylase/trypsin inhibitor - maize c. Species: Zea mays (maize) c. Species: Zea mays (maize) c. Species: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 07-Feb-1997 c. Accession: A29541, A3174 R. Richardson, M.; Valdes-Rodriguez, S.; Blanco-Labra, A. Nature 327, 432-434, 1987 A. Mature 327, 432-434, 1987 A. Mature 327, A32-434, 1987 A. Ma
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A;Residues: 1-316 <SIN>
A;Cross-references: EMBL:X15387; NID:97293; PIDN:CAA33445.1; PID:97294
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                                                                                                                  13;
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     Length 227;
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                                                                                                             18; Indels
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Pred. No. 10;
Score 68.5; DB 2;
Pred. No. 5.2;
9; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-206 <RIC>
R; Vigers, A.J.; Roberts, W.K.; Selitrennikoff, C.P.
submitted to the Protein Sequence Database, May 1991
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15.4%; Score 64.5; DE
Best Local Similarity 24.6%; Pred. No. 18;
Matches 17; Conservative 7; Mismatches
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mutants block sporulation after engulfment spoilIAE - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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Pred. No.
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nes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: spolliAE
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C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C; C; Cacession: H69937
C; Bron, S; Broullet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; Chc
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E.
A; Alathich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E.
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Koetter, D.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, R.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T. M.; Pathors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seronion,
A; Winters: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Tosato, V.; Uchiyama,
A; Withors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.;
A; Heference number: A6588; WILD:98044033; PMID:9384377
A; Accession: H69937
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         high-potential iron sulfur protein isoform 2 - Ectothiorhodospira vacuolata N.Alternate names: HiPIP protein C.Species: Ectothiorhodospira vacuolata C.Species: Ectothiorhodospira vacuolata C.Species: Ectothiorhodospira vacuolata C.Saccession: 841614
R.Ambler, R.P.; Mayer, T.E.; Kamen, M.D.
R.Ambler, R.P.; Mayer, T.E.; Kamen, M.D.
Arch. Blochen. Blophys. 308, 78-81, 1994
A.Title: Amino acid sequences of two high-potential iron sulfur proteins (HiPIPs) from A; Reference number: 841611; MUID: 94145107; PMID: 8311477
A.Accession: 841614
A.Molecule type: protein
A.Residues: 1-71 cAMB>
A.Residues: 1-71 cAMB>
C.Superfamily: high potential iron-sulfur protein
C.Superfamily: high potential iron-sulfur protein
C.Superfamily: high potential iron-sulfur protein; metalloprotein
F;34,37,51,65/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 LDGDQPADRPAERMQDDISSDEHPLFDKRQNCCN-------GGCS-----S 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 MMSKLGVLLTVCLLLFPLTALP--LDGDQPADRPAERMQDDISS--DEHPLFD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.2%; Score 64; DB 2; Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.2%; Score 64; DB 2; Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: Bacillus subtilis hypothetical protein ypjP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 68; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-203 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GWC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 KWC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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C; Accession: H6971

R; Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Ber

C; Bron, S; Broulliet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M;

A; Ehrlich, S.D; Emmerson, P.T; Entian, K.D; Errington, J; Fabret, C; Ferrari,

Nature 390, 249-256, 1997

A; Authors: Foulgar, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Gal

A; Authors: Lauber, D; Krogh, S; Kumano, M; Kurita, K; Lapidus, A; Landino

A; Authors: Lauber, J; Hazarevic, V; Lee, S.M; Levine, A; Liu, H; Masuda, S; Mulo

N; Authors: Lauber, J; Hazarevic, W; Lee, S.M; Levine, A; Liu, H; Masuda, S; Mulo

N; Rieger, M; Rivolta, C; Rocha, E; Roche, B; Rose, M; Sadale, Y; Ssato, T; Scanl

Rieger, M; Rivolta, C; Rocha, E; Roche, B; Rose, M; Sadale, Y; Ssato, T; Scanl

A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Sekjuchi, J; Sekowska, A; Se

A; Authors: Schleich, S; Cannamoto, H; Yamane, K; Yasumoto, K; Yata, K; Yoshida

A; Authors: Yoshikawa, H.F; Zumstein, E; Yoshikawa, H; Danofin, A

A; Title: The complete genome Sequence of the Gram Positive Dacterium Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:U61754; NID:g1432157; PID:g1432158
A;Cross-references: GB:U61754; NID:g1432157; PID:g1432158
C;Comment: This protein is a glycoprotein belonging to the transforming growth factor ng embryonic development and sex determination:
F;1-20/Domain: signal sequence #status predicted <SIG>F;1-644/Product: anti-Muellerian hormone homologue #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1.405 <KUN>
A;Cross-references: GB:299116; GB:AL009126; NID:g2634723; PIDN:CAB14370.1; PID:e1\u00a435
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 02-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 04-Mar-2000
C;Accession: JC5119
R;Neeper, M.; Lowe, R.; Galuska, S.; Hofmann, K.J.; Smith, R.G.; Elbrecht, A. Gene 176, 203-209, 1996
A;Title: Molecular cloning of an avian anti-Muellerian hormone homologue.
A;Reference number: JC5119
A;Accession: JC5119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 LGVAILICIAAFPAIKVLSLAFIYKLAAAILQPLGGG-----PVITCLDVISKSGHLYFC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PLDGDQPADRPAERMQDDISSDEHPLFD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.2%; Score 64; DB 2; Length 405; 23.8%; Pred. No. 25; Live 10; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-mullerian hormone homolog precursor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
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RESULT 11

RESULT 9 H69711

Gaps

10;

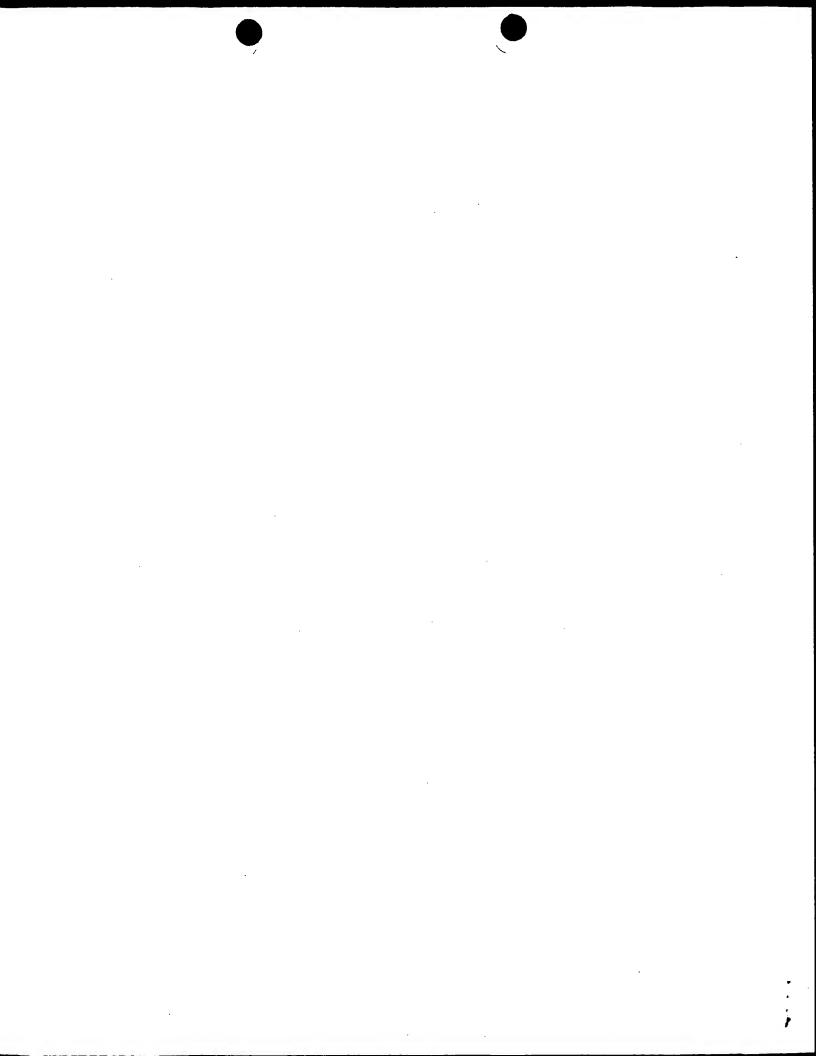
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A)Cross-references: GB:AE005174; NID:g12516009; PIDN:AAG56926.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N'Alternate names: seminal vesicle secretory protein 109 (svSP109)
(Species: Bos primigenius taurus (cattle)
(C) Date: 14-Nov-1983 #sequence_revision 05-May-1995 #text_change 22-Jun-1999
(C) Accession: S18404; S45010; A31852; A61564; A03256; S59518; S48674
(R) Bracuer, C.; Scheit, K.H.
(R) Biochim: Biochimys. Acta 1090, 259-260, 1991
(A) Title: Characterization of the gene for the bovine seminal vesicle secretory protein A). Reference number: S18404; MUID: 92031704; PMID: 1932121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-134 <BRA
A; Cross-references: GB:X60495; NID:929; PIDN:CAA43021.1; PID:9833775
A; Cross-references: GB:X60495; NID:929; PIDN:CAA43021.1; PID:9833775
B; Braeuer, C.C.; Kleine Kuhlmann, J.J.; Hanes, J.J.; Scheit, K.K.
B; Braeuer, C.C.; Kleine Kuhlmann, J.J.; Hanes, J.J.; Scheit, K.K.
A; Description: Structure and promoter analysis of the genes for bovine SVSP109 and se
A; Reference number: S45010
                                                                                                                                                                                                                                                                           6 KLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRONCCNGGCSSKW 65
                                                                                                                                                                                                                                                                                                                      39 RCGLLMAICLCLVSFSGYAATGKSDAQIKKEIIKESIES--YP----GNC---ACPYNH 88
                                                                                                                                                                                 15.0%; Score 63; DB 2; Length 130;
                                                                                                                                                                                                                            30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the function of this protein is not known
                                                                                                                                                                                                   27.1%; Pred. No. 13;
ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seminal fluid protein PDC-109 precursor - bovine
                                                                                                                                                                                                Local Similairus
hes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 26-134 <FSC>
          A; Molecule type: DNA
A; Residues: 1-130 <STO>
                                                                                                                                                                                                                                                                                                                                                                     66 CRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                  89 ARNGSRCGGR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-134 <BR2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S45010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A03256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A31852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A61564
                                                                                                                             A; Gene: Z2994
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                                                           Óγ
                                                         Cybate: 18-04-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
Cybate: 18-Uul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
Cybate: 18-Uul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
Cyaccession: A90960
RyHayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A; Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary
A; Residues: preliminary
A; Residues: 1-93 < HAX>
A; Cross-references: GB:BA000007; PIDN:BAB36072.1; PID:g13362117; GSPDB:GN00154
C;Genetics:
A;Gene: ECS2649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ECs2649 (imported] - Escherichia coli (strain 0157:H7, substrain Rİ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                A.Cross references: GB:AE005673; NID:913424080; PIDN:AAK24492.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC2521
sensor histidine kinase/response regulator [imported] - Caulobacter crescentus
                    C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 GVLLOV-LLLYRLTHOMVAAPLEALADAQQGDPAAARPFEARPDEIGSLARALRRQRE 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 KLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCSSKW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 GVLLTVCLLLFPLT----ALPLD------GDQPADRPAERMQDDISSDEHPLFDKRQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.0%; Score 63; DB 2; Length 93; 27.1%; Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 49;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    15.1%; Score 63.5; 40.7%; Pred. No. 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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es 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 CRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 ARNGSRCGGR 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
B85808
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A:Residues: 1-134 (KEM)
A:Cross-references: GB:M22244; NID:g163734; PIDN:AAA30766.1; PID:g163735
A:Cross-references: GB:M22244; NID:g163734; PIDN:AAA30766.1; PID:g163735
B:Schaft, K.H.; Kemme, M.; Aumueller, G.; Seitz, J.; Hagendorff, G.; Zimmer, M.
Biosci. Rep. 8, 589-608, 1988
A:Title: The major protein of bull seminal plasma: biosynthesis and biological functi
A:Reference number: A61564; MUID:89207711; PMID:2468369
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Biol. Chem. Hoppe-Seyler 376, 631-636, 1995
A:Title: The gene for the major protein (SVSP109) of bovine semen: structure and prom A; Reference number: SS9518; MUID:96145730; PMID:8690633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Cloning and sequence analysis of a CDNA from seminal vesicle tissue encodi
A,Reference number: A31852; MUID:89152746; PMID:3229283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: residues 49-86 and 94-134 form two structurally similar domains, A and B,
A;Cross-references: EMBL:233621; NID:g488602; PIDN:CAA83915.1; PID:g488603
Kremme, M.; Schell, K.H.
DNA 7, 595-599, 1988
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A; Cross-references: EMBL:233621; NID:9488602; PIDN:CAA83915.1; PID:9488603
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
A; Note: only a part of the nucleic acid sequence is shown; only a part of the translatid
R; Calvete, J.J.; Raida, M.; Sanz, L.; Wempe, F.; Scheit, K.H.; Romero, A.; Toepfer-Peter
FEBS Lett. 350, 203-206, 1994
A; Title: Localization and structural characterization of an oligosaccharide O-linked to
                                                                                                                                                                                                                                                                                                                                                                                   Concerns 26/1; 46/1; 90/1
Cisuperfamily: seminal fluid protein PDC-109; fibronectin type II repeat homology Cisuperfamily: seminal fluid protein PDC-109; fibronectin type II repeat homology F:1-25/Domain: signal sequence #status predicted <SIG>F:26-134/Product: seminal fluid protein SVSP109 #status experimental <MAT>F:249-86/Domain: fibronectin type II repeat homology <2FO>F:34-ADOmain: fibronectin type II repeat homology <2PO>F:36/Binding site: carbohydrate (Th) (covalent) (partial) #status experimental F:49-73,63-86,94-119,108-134/Disulfide bonds: #status experimental
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A;Nolecule type: DNA
A;Residues: 1-523 <NIL>
A;Cross-references: EMBL:282268; PIDN:CAB05197.1; GSPDB:GN00022; CESP:F52B11.1
A;Experimental source: clone F52B11
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T22484
R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQD---DISSDEHPLFD-----KR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 4
A;Introns: 57/1; 151/3; 268/3; 372/2; 482/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F52B11.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.0%; Score 63; DB 1; Length 134; 25.5%; Pred. No. 13; ative 11; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 2; Length 523;
Pred. No. 38;
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                                                                                                                                                                                                                                             A; Reference number: S48674; MUID:94350099; PMID:8070564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F52B11.1 - Caenorhabditis elegans
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A;Reference number: 219569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- RDHARC 72
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                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 26-35,'X',37-56;60-89 <CAL>
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Best Local Similarity 32.1%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.58
Matches 24; Conservative
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A; Residues: 1-134 <BR3>
                                                                                                                                                                                                                                                                             A; Accession: S48674
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 10, 2003, 08:32:27 : Search time 12.3913 Seconds (without alignments) 251.041 Million cell updates/sec Run on:

US-09-910-009A-210 420 1 GSMMSKLGVLLTVCLLLFPL..........CCNGGCSSKWCRDHARCCGR 75 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ipti	. O24006 i antimicro	C	radi	couns	Conus	conns	zea ma	zea	P14326 dictyosteli			P49782 bacillus su	bos tauru				_	P20721 lycopersico	P28797 cavia porce			mus muscul					homo sapie		Q14508 homo sapien			57 rhizobium	531
SUMMARIES	ID	AMP_IMPBA	CXA1_CONST	COW_CONRA	COW1_CONTE	CXM3_CONPU	COW3_CONTE	ZEAM_MAIZE	IAAT_MAIZE	VSH5_DICDI	HPI2_ECTVA	YPJP_BACSU	S3AE_BACSU	SFP1_BOVIN	COW2_CONTE	YKR1_CAEEL	GPCR_LYMST	COM_CONSE	CYSL_LYCES	GRN_CAVPO	RELB_HUMAN	Y734_CHLPN	DLK_MOUSE	FA7_HUMAN	IAA2_HORVU	Ø	TRY1_ANOGA		LDLR_CRIGR	WFD2_HUMAN	FA7_RABIT	YOX4_CAEEL		WFD2_RABIT
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FA7_MOUSE	TSCI_HOMAN	CALM_BLAEM	RSP4_ECHGR	V290_ASFL5	M172 HUMAN	GRP_TOBAC	RGSJ HUMAN	LEG8_HUMAN	THRB_BOVIN	HG2A_RAT	OXLA_NEUCR
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57.5	. !	27	57	57	22	56.5	56.5	56.5	56.5	56	26
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ALIGNMENTS

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                 Plant defense; Cleavage on pair of basic residues; Repeat; Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 MSKLGVLLTVCLLLFPLTAL-----PLDGDQPADRPAE----RMQDDISSDEHPLFD 51
                                                                                                                                                                                                                                                                                                 (PROBABLE).
                                                                                                                                                                                                                                                                                                                       (PROBABLE).
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PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
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Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.4%; Score 73; DB 1; Length 333; 28.0%; Pred. No. 0.83;
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BY SIMILARITY.
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W; A3B2BE2D9184407D CRC64;
                                                                                                                                                                           BASIC PEPTIDE AMP1-1.
                                                                                                                                                                                                                          BASIC PEPTIDE AMP1-3.
                                                                                                                                                                                                  BASIC PEPTIDE AMP1-2.
                                                                                                                                       ACIDIC PEPTIDE 1.
BASIC PEPTIDE AMP3.
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                                                                                                                                                                                                                                                                          BASIC PEPTIDE AMP4.
                                                                                                                                                                                                                ACIDIC PEPTIDE 4.
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5-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                               ACIDIC PEPTIDE 2.
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                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-conotoxin SI precursor (S1). Conus striatus (Striated cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom duct;
MEDLINE=20037955; PubMed=10573284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37259 MW;
                                                                                         EMBL; Y14369; CAA74738.1; -.
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122
164
168
212
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333 AA;
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                                                                                                                 Fungicide; Signal. SIGNAL 1
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75
103
123
149
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P15471;
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-i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Expressed by the venom duct.
-i- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Contryphan precursor [Contains: Contryphan-R (Bromocontryphan); [des-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 VLLTVCLLLFPLTALPLDGDQPADRPAERMQD---DISSDEHPLFDKRQNCCNGGCSSKW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ11
SEQ1ANCE FROM N.A., SEQUENCE OF 55-62, SYNTHESIS OF BROMOCONTRYPHAN,
AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 55-62, SYNTHESIS OF CONTRYPHAN, AND MASS SPECTROMETRY.
                                                                                                                                                                       Biochemistry 27:7102-7105(1988).

Biochemistry 27:7102-7105(1988).

-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus
                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION (G-63 PROVIDE AMIDE GROUP). B104B80ccD7c3B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jimenez E.C., Craig A.G., Watkins M., Hillyard D.R., Gray W.R., Gulyas J., Rivier J.E., Cruz L.J., Olivera B.M.; "Bromocontryphan: post-translational bromination of tryptophan."; Biochemistry 36:989-994(1997).
                                                                                                        Zafaralla G.C., Ramilo C., Gray W.R., Karlstroem R., Olivera B.M.,
                                                                                                                                       "Phylogenetic specificity of cholinergic ligands: alpha-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.3%; Score 72.5; DB 1; Length 64; 31.4%; Pred. No. 0.22; tive 11; Mismatches 24; Indels
Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.; "Conopeptides from Conus striatus and Conus textile by cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=61198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97067006; PubMed-8910408;
Jimenez E.C., Olivera B.M., Gray W.R., Cruz L.J.;
"Contryphan is a D-tryptophan-containing Conus peptide.";
J. Biol. Chem. 271:28002-28005(1996).
                                                                                                                                                                                                                                                                                                                                      Acetylcholine receptor inhibitor; Signal; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                   ALPHA-CONOTOXIN SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 AA.
                                                                                                                                                                                                                                                                                         FAMILY.
PIR; A28953; A28953.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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MEDLINE=97185706; PubMed=9033387;
                                                                                              MEDLINE=89062448; PubMed=3196703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus radiatus (Rayed cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  7164 MW;
                                                Peptides 20:1139-1144(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                     49
62
56
62
62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 CRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ----- SCGR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AA;
                                                                                                                                                                                                                              inhibit them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COW_CONRA
P58786;
                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                  SEQUENCE
                                                                                                                                  Cruz L.J
                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDE
                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                          PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COW_CONRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
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4;

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Jimenez E.C., Watkins M., Juszczak L.J., Cruz L.J., Olivera B.M.; Contryphans from Conus textile venom ducts.";
Toxicon 39:803-808(2201).
-!- SUBCELLULAR LOCATION: Secreted.

MEDLINE=21065889; Pubmed=11137539;

TISSUE SPECIFICITY: Expressed by the venom duct. MASS SPECTROMETRY: MW=966.5; METHOD=MALDI.

-!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.

```
4;
                                                                                                                                                                                                                               isomerization at Cys-56-Hyp-57.
-!- PTM: The differences between contryphan-R and bromocontryphan lies in the state of bromination of Trp-61.
                                                     "Solution structure of contryphan-R, a naturally occurring disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BROMINATION (IN ISOFORM BROMOCONTRYPHAN).
                                                                bridged octapeptide containing D-tryptophan: comparison with protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 MSKLGVL-LTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGKLTILVLVAAVLLSAQVMVQGDGDQPADRNA-----VPRDDNP------GGAS 44
                                                                                                                                                                                                                                                                                                                 -!- MASS SPECTROMETRY: MW=933.3; METHOD=Electrospray; RANGE=ISOFORM [DES-GLY1]CONTRYPHAN-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxin; Hydroxylation; D-amino acid; Amidation; Signal; Bromination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROVIDE AMIDE GROUP).
                                                                                                                                            Pallaghy P.K., He W., Jimenez E.C., Olivera B.M., Norton R.S.; Structures of the contryphan family of cyclic peptides. Role of electrostatic interactions in cis-trans isomerism."; Biochemistry 39:12845-12852(2000).
-- SUBCELLULAR LOCATION: Secreted.
-- TISSUE SPECIFICITY: Expressed by the venom duct.
                                                                                                                                                                                                                                                                                                                                            -!- MASS SPECTROMETRY: MW=1070.5; METHOD=MALDI; RANGE=ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 63;
                           Pallaghy P.K., Melnikova A.P., Jimenez E.C., Olivera B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Indels
                                                                                                                                                                                                                                                                                      MASS SPECTROMETRY: MW-990.3; METHOD=Electrospray;
RANGE=ISOFORM CONTRYPHAN-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION (G-63 PROVIDE
5FAE62CDB6B016B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [DES-GLY1]CONTRYPHAN-R
                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.28
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-TRYPTOPHAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTRYPHAN-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                     STRUCTURE BY NMR.
MEDLINE=20496763; PubMed=11041849;
           MEDLINE=99400497; PubMed=10471307;
                                                                                           Biochemistry 38:11553-11559(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6667 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 SK-----WC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 GKFMNVLRRSGCPWEPWC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
54
62
62
62
57
58
                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 1QFB; 29-SEP-99.
PDB; 1DG0; PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                        BROMOCONTRYPHAN.
                                                                                                                                                                                                                                                                                                                                                                                 PIR; A58511; A58511
PIR; B58511; B58511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
55
55
57
57
62
                                        Norton R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
MOD_RES
SEQUENCE
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δλ
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3;

16; Indels 17; Gaps

DB 1; Length 63;

Pred. No. 0.35;

16.8%; 34.98;

6801 MW;

63 AA;

SEQUENCE Query Match

8; Mismatches Score 70.5;

22; Conservative

Matches

63 SKW 65

qq δy

ŏ

Local Similarity

DA25657C06A05EED CRC64;

SIMILARITY)

4 MSKLGVLLTVCL-LLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCS 62

D-AMINO ACID (BY SIMILARITY). AMIDATION (G-63 PROVIDE AMIDE GROUP) (BY

SIMILARITY).

CONTRYPHAN-TX (BY SIMILARITY)

BY SIMILARITY.

POTENTIAL

HYDROXYLATION (BY

23 54 57 58 58

24 55 57 58 62

PEPTIDE MOD_RES MOD_RES MOD_RES

SIGNAL PROPEP

Hydroxylation; D-amino acid; Amidation; Signal.

EMBL; AF166323; AAF82243.1; -.

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Safo P., Rosenbaum T., Shcherbatko A., Choi D.-Y., Han E., Toledo-Aral J.J., Olivera B.M., Brehm P., Mandel G.; "Distinction among neuronal subtypes of voltage-activated sodium channels by mu-conotoxin PIIIA."; J. Neurosci. 20:76-80(2000).
                                                                                                                                                                                                                                                                                        Gray W.R.,
                                                                                                                                                                                                                                                                                  Shon K.-J., Olivera B.M., Watkins M., Jacobsen R.B., Gray W.R. Floresca C.Z., Cruz L.J., Hillyard D.R., Brink A., Terlau H.,
                                                                                                                                                                                                                                                                                                                          "mu-Conoctoxin PIIIA, a new peptide for discriminating among tetrodotoxin.sensitive Na channel subtypes.";
                                                                                                                                                                Conus purpurascens (Purple cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A., SYNTHESIS, AND MUTAGENESIS
                                                                                                                      (Rel. 41, Last sequence update)
                                                                                                                                                Mu-conotoxin PIIIA precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                       BINDING TO NEURONAL SODIUM CHANNELS.
                                                                                                                                                                                                                                                                                                                                                             J. Neurosci. 18:4473-4481(1998).
                                                                                                        (Rel. 41, Created)
                                                                          STANDARD;
                                                                                                                                                                                                                                                    TISSUE=Venom duct;
                                                                                                                                                                                                            NCBI_TaxID=41690;
                                                                                                                                      (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=10627583;
                                                                                                                                                                                                                                                                    PubMed=9614224;
                                                                                                                                                                                                                                                                                                                 Yoshikami D.;
                                                                                                      15-JUN-2002
 45 EKF 47
                                                                                                                                    15-JUN-2002
                                                                                                                    15-JUN-2002
                                                                         CXM3_CONPU
                                                                                        P58925
                                           RESULT 5
CXM3_CONPU
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Conus textile (Cloth-of-gold cone). Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neogastropoda; Conoidea; Conidae; Conus.

15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)

Contryphan-Tx precursor.

63 AA

PRT;

STANDARD;

COW1_CONTE Q9NDA7;

COW1_CONTE

RESULT

SEQUENCE FROM N.A., SYNTHESIS, AND MASS SPECTROMETRY.

TISSUE=Venom duct;

NCBI_TaxID=6494;

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KW
FT
FT
FT
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SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ?
            Nielsen K.J., Watson M., Adams D.J., Hammarstroem A.K., Gage P.W., Hill J.M., Craik D.J., Thomas L., Adams D., Alewood P.F., Lewis R.J.; "Solution structure of mu-conotoxin PIIIA, a preferential inhibitor of persistent TTX sensitive sodium channels."; J. Biol. Chem. 277:0-0(2002).
-: FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
                                                                                                   roxin; Neurotoxin; Sodium channel inhibitor; Hydroxylation; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                   R->A: DECREASE IN AFFINITY TO CHANNEL F0E19F45BC97AC13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom duct;
MEDLINE=21065889; PubMed=11137539;
Jimenez E.C., Matkins M., Juszczak L.J., Cruz L.J., Olivera B.M.;
"Contryphans from Cours textile venom ducts.";
Toxicon 39:803-808(2001).
-1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-26 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus textile (Cloth-of-gold cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70; DB 1; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., SYNTHESIS, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- TISSUE SPECIFICITY: Expressed by the venom duct.
-:- MASS SPECTROMETRY: MW=880.5; METHOD=MALDI.
-:- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
                                                                                                                                                                                                                                                                                                        MU-CONOTOXIN PILIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        (PROBABLE)
                                                                                                                                                                                                                                                                                         PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKRQNCCNG---GCSSKWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EKRQRLCCGFPKSCRSRQCKPH-RCCGR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                          Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leu-contryphan-Tx precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                        25
19
24
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-6494;
       PubMed=12006587;
                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGEN
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                                                                                                                                                                                                                                                                             NON TER
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                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-96133724; PubMed-8548448;
Batalia M.A., Monzingo A.F., Ernst S., Roberts W., Robertus J.D.;
Batalia M.A., Monzingo A.F., Ernst S., Roberts W., Robertus J.D.;
The crystal structure of the antifungal protein zeamatin, a member of the thaumatin-like, PR-5 protein family.";
Nat. Struct. Biol. 3:19-23(1996).
-!- FUNCTION: HAS ANTIFUNGAL ACTIVITY. INHIBITS CANDIDA ALBICANS AND TRICHODERMA RESEL; MARGINAL INHIBITION OBSERVED AGAINST
ALTERNARIA SOLANI AND NEUROSPORA CRASSA.
-!- SIMILARITY: BELONGS TO THE THAUMATIN FAMILY.
                                                                                                                           D-AMINO ACID (BY SIMILARITY).
AMIDATION (G-63 PROVIDE AMIDE GROUP) (BY
                                                                                                                                                                                                                                                                                                                                                                  4 MSKLGVL-LTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCS 62
                                                                                                                                                                                                                                                                                                                     31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Malehorn D.E., Borgmeyer J.R., Smith C.E., Shah D.M.; "Characterization and expression of an antifungal zeamatin-like protein (Zlp) gene from Zea mays."; Plant Physiol. 106:1471-1481(1994).
                                                                                            LEU-CONTRYPHAN-TX (BY SIMILARITY).
                                                                                                                                                                                                                                                          Score 68.5; DB 1; Length 63;
Pred. No. 0.58;
7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roberts W.K., Selitrennikoff C.P.; "Zeamatin, an antifungal protein from maize with membrane-permeabilizing activity."; J. Gen. Microbiol. 136:1771-1778(1990).
                                                                                                                                                                                                          2A910957B7E44BB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 AA
                                                                         BY SIMILARITY
                                                                                                                                                                                    SIMILARITY)
EMBL, AF166324; AAF82244.1; -.
Toxin; D-amino acid; Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-cv. B73; TISSUE-Seed;
MEDLINE-95148737; PubMed-7846159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; Li
Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U06831; AAA92882.1; -. PIR; A33174; A33174.
                                                                                                                                                                                                                                                                        16.3%;
                                                                                                                                                                                                                                                                                               29.5%;
                                                                                                                                                                                                                   6678 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 GKLMDVLRPKKCVLYPWC 62
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                     52
52
53
53
62
63
                         Toxin; D-amino acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zeamatin precursor.
                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-48.
                                                                                                                                                                                                                   63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZEAM_MAIZE
P33679:
                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                           Query Match
                                                                              PROPEP
PEPTIDE
                                                                                                                                    MOD_RES
MOD_RES
                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZEAM_MAIZE
                                                                                                                                                                                                                                                                                                                                   Matches
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; 2ea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun., 182:1-5(1992).
-!- FUNCTION: INHIBITS BOTH TRYPSIN AND ALPHA-AMYLASE. INHIBITS THE GROWTH OF SOME PLANT FUNGAL PATHOGENS.
-!- SIMILARITY: BELONGS TO THE THAUMATIN FAMILY.
PIR: A29581; A29581.
HSSP; P33679; 1DU5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huynh Q.K., Borgmeyer J.R., Zobel J.F.;
"Isolation and characterization of a 22 kDa protein with antifungal
properties from maize seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 PLTALPLDGDQPADR-----PAERMQDDISSDEHPLFDKRQNCCNGGCSS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.3%; Score 68.5; DB 1; Length 227; 29.8%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Richardson M., Valdes-Rodriguez S., Blanco-Labra A.; "A possible function for thaumatin and a TMV-induced protein Suggested by homology to a maize inhibitor."; Nature 327:432-434(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23999 MW; 33ABFE0B1EB781E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-amylase/trypsin inhibitor (Antifungal protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                              Promission Programments Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                            ZEAMATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92117998; PubMed=1731773;
                      MaizeDB; 78797; -. InterPro; IPR001938; Thaumatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                       227
226
    PDB; 1DU5; 02-FEB-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAAT_MAIZE
P13867;
                                                                                                                                                                                                                                                           DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAAT_MAIZE
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 LLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCSSKWC----- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                             Singleton C.K., Manning S.S., Ken R., Submitted Marigology of the EMBL/GenBank/DDBJ databases.
-!- DEVELOPMENTAL STAGE: THIS PROTEIN IS EXPRESSED IN GROWING CELLS AND DEACTIVATED UPON THE INITIATION OF DEVELOPMENT.
-!- SIMILARITY: BELONGS TO THE "GDXG" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                              19 PLTALPLDGDQPADR------PAERMQDDISSDEHPLFDKRQNCCNGGCSS 63
                                                                                                                                       19; Indels 13;
                                                                                                             Score 65.5; DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.4%; Score 64.5; DB 1; Length 316; 24.6%; Pred. No. 6.5; tive 7; Mismatches 14; Indels 31
 BY SIMILARITY.
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BY SIMILARITY.
Y -> M (IN REF. 2).
Y -> M (IN REF. 2).
W; 6C73ElBACAE090DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
876C87A360F3C936 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                         Pred. No. 3.5;
8; Mismatches
                                                                                                                                                                                                                                                               PRT; 316 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S07569; S07569.
DictyDb; DD01021; cinB.
InterPro; IPR000379; Ser_estrs_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
194 BY BY 177 BY 142 BY 155 BY 164 BY 22075 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 PO
165 PO
36053 MW;
                                                                                                                                                                                                                                                                                                                            Vegetative specific protein H5 CINB OR H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPI2_ECTVA STANDARD; P
P38524;
01-0CT-1994 (Rel. 30, Created)
                                                                                                            15.6%;
                                                                                                                         29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X15387; CAA33445.1; -.
                                                                                                                                    17; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                                             STANDARD;
118
124
132
146
156
206 AA;
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165
316 AA;
                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AX3;
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                         DISULFID
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DISULFID
                                                                 CONFLICT
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ACT_SITE
SEQUENCE
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               DISULFID
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63 GWC 65
   64 KWC 66
                                    YPJP_BACSU
                                RESULT 11
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    δλ
                                                                                                                                                                                                                                                                                                                                                                                       22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 ------ GGCS----- 63
                                                                                                                                                                                                                                                                                                                                                                                                       Ambler R.P., Meyer T.E., Kamen M.D.;
Amino acid sequences of two high-potential iron sulfur proteins
(Hipips) from the moderately halophilic purple phototrophic bacterium
                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Ectothiorhodospiraceae;
Ectothiorhodospira.
NCBL_TaxID=1054;
                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 71;
                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
                                                                                                                                                                                                                  3D-structure.
(4FE-4S).
(4FE-4S).
(4FE-4S).
(4FE-4S).
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
High potential iron-sulfur protein isozyme 2 (HiPIP 2).
                                                                                                                                                                                                                                                                                                                                                                 EE2FA335594898C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                       IRON-SULFUR (
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IRON-SULFUR (
IRON-SULFUR (
                                                                                                                                                                                                                                                                                                                                                                                  No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                  25 LDGDQPADRPAERMQDDISSDEHPLFDKRQNCCN--
                                                                                                                                                                                                                  Electron transport; Iron-sulfur; 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                                              Score 64;
                                                                                     Ectothiorhodospira vacuolata.";
Arch. Biochem. Biophys. 308:78-81(1994).
                                                                                                    X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                       PDB; IHPI; 30-APR-94.
InterPro; IPR000170; Hipot_ironsulf.
                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                          STRAIN=Beta-1 / DSM 2111;
MEDLINE=94162261; PubMed=8117708;
                                                              MEDLINE=94145107; PubMed=8311477;
                                                                                                                                                                                                        PRINTS; PR00374; HIPIPFRDOXIN.
PROSITE; PS00596; HIPIP; 1.
                                                                                                                                                                                                                                                                                                                                                                             15.2%;
                       Ectothiorhodospira vacuolata.
                                                                                                                                                                                                                                                                                                                                                                  7819 MW;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                         STRAIN=Beta-1 / DSM 2111;
                                                                                                                                                                                                  Pfam; PF01355; HIPIP; 1
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                  71 AA;
                                                                                                                                                                                  (HIPIP) FAMILY
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Best Local Simi
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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REA KURST F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Acevedo V., Berterro M.G., Bessleres P., Bolotin A., Borchert S.,

RA Acevedo V., Berterro M.G., Bessleres P., Bolotin A., Borchert S.,

RA Acevedo V., Berterro M.G., Erans A., Braun M., Brignell S.C., Bron S.,

RA Borriss R., Boursier L., Frans A., Braun N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,

RA Eritz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,

RA Fritz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Agandt A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Moone D. O'Rellly M., Porthelle D., Porwollik S., Prescott A.M.,

RA Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadaie Y.,

RA Schluchi J., Schola E., Roche B., Rose M., Sadaie Y.,

RA Schuchi A., Tamakoshi A., Tanaka T., Terkhashi H., Takemaru K.,

RA Tosato V., Uchiyama S., Vandeler E., Wedler E., Vasarotti A.,

Vairi A., Wambutt R., Wedler E., Wedler E., Wedler E., Vasarotti A.,

RA Voshida K., Yoshikawa H.F., Zummeten E., Yoshikawa H., Danchin A.,

RA Voshida K., Yoshikawa H.F., Zummeten E. Yoshikawa H.P., Vasumoto H., Yasumoto K., Yatu M.,

RA Voshila K., Yoshikawa H.F., Zummeten E., Yoshikawa H., Danchin A.,

RA H., Wandler S., Wilpet C., Yatu H.,

RA H., Wandler S., Wilpet C., Yatu H.,

RA Wilters P., Wilpet S., Wilpet S.,

RA Wilters P., Willer S., Willer S., Waller S.,

RA Wilters P., Wilpet S.,

RA Wilters P., Willer S., Wandeler E., Wedler E., Wedler S.,

RA Wilt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iwakura M., Kawata M., Tsuda K., Tanaka T.; "Nucleotide sequence of the thymidylate synthase B and dihydrofolate reductase genes contained in one Bacillus subtilis operon."; Gene 64:9-20(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96349105; Pubmed-8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.
                                                                                                                                                                                                                                                                                                                                                Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last annotation update)
Hypothetical protein ypjP.
203 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88284366; PubMed=2840350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:249-256(1997).
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-168 / Marburg;
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                                                                                                                                                                                                                                                                                                                             Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1423;
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         YPJP_BACSU
P54172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L.V., Erans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Cadawell B., Capano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Enizor F., Devine K.D., Errington J., Rabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Adhim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Alliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Andria B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Odiwas V., Oudega B., Park S.H., Prescean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                  15.2%; Score 64; DB 1; Length 203; 35.8%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gonzy-Treboul G., Stragier P.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                          6F9334D92434D3BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 AA
                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                   EMBL; M20012: -; NOT ANNOTATED_CDS.
Subtilist; BG11616; ypjp.
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=168 / JH642;
MEDLINE=97124195; Pubmed=8969508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stage III sporulation protein AE.
                                                                                                                                                                                                                                                                      203 AA; 23663 MW;
                                                                                                                                     EMBL; L77246; AAA96632.1; -. EMBL; Z99115; CAB14102.1; -.
                                                                                                                                                                                                                                                                                                                                                              19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=168 / JH642;
Guerout-Fleury A.M., G
Submitted (SEP-1995) t
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S3AE_BACSU
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P49782;
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                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Saklguchi J., Schleich S., Seror P., Shin B.S., Soldo B., Sorokin A., Tamakoshi A., Tanakashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tagononi A., Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A., Viari A., Nambutt R., Wedler E., Wedler H., Weitzenegger T., Winter P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Voshikawa H.F., Danchin A., The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G -> E (IN REF. 1).
GHLYFCSSRHCVSHVFFKPYCHNHSRKPHDDDEMKEAG ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIYIFAALAIVSLMFFLSLTVIITAGNLTMMM (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 LGVAILICIAAFPAIKVLSLAFIYKLAAAILQPLGGG-----PVITCLDVISKSGHLYFC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and sequence analysis of a cDNA from seminal vesicle tissue encoding the precursor of the major protein of bull semen."; DNA 7:595-599(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
01-AGC-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Seminal plasma protein PDC-109 precursor (Seminal vesicle secretory
protein 109) (SVSP109) (BSP-A1 and BSP-A2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                               Nature 390:249-256(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.2%; Score 64; DB 1; Length 405; 23.8%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F8ED649F38EB544F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Complete proteome.
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MEDLINE=89152746; PubMed=3229283;
Kemme M., Scheit K.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 AA; 43842 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 SSRHCVSHVFFKPYCHNHSR 392
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U35252; AAA76724.1; -. EMBL; D84432; BAA12564.1; -. EMBL; Z99116; CAB14370.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Subtilist; BG11412; spoilians. Sporulation; Transmembrane; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 KRONCCNGGCSSKWCRDHAR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
160
192
229
268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
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172
209
248
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P02784;
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J. Mol. Biol. 223:281-298(1992).
-!- FUNCTION: COULD ENHANCE THE FERTILIZING CAPACITY OF BULL
SPERMATOZOA UPON INTERACTION WITH HEPARIN-LIKE GIYCOSAMINOGIYCANS
PRESENT IN THE FEMALE GENITAL TRACT. EXHIBITS BOTH SIMULATORY AND
INHIBITORY ACTIONS ON THE RELEASE OF PITUITARY GONADOTROPINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence-specific 1H NWR assignments and structural characterization of bovine seminal fluid protein PDC-109 domain b.";
Biochemistry 30:1663-1672(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MICROHETEROGENEITY ACCOUNT FOR DIFFERENCES BETWEEN BSP-A1 AND BSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerwig G.L., Calvete J.J., Toepfer-Petersen E., Vliegenthart J.F.G., "The structure of the O-linked carbohydrate chain of bovine seminal plasma protein PDC-109 revised by H-NMR spectroscopy A correction."; FEBS Lett. 387:99-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-83256590; PubMed-6870895;
Esch F.S., Ling N.C., Boehlen P., Ying S.Y., Guillemin R.;
"Primary structure of PDC-109, a major protein constituent of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Refined solution structure and ligand-binding properties of PDC-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Localization and structural characterization of an oligosaccharide O-linked to bovine PDC-109. Quantitation of the glycoprotein in seminal plasma and on the surface of ejaculated and capacitated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94350099; PubMed=8070564;
Calvete J.J., Raida M., Sanz L., Wempe F., Scheit K.H., Romero A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER.
IISSUE SPECIFICITY: MAJOR COMPONENT OF SEMINAL PLASMA.
PTM: O-GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
MODIFIED WITH A SIALIC ACID RESIDUE (MACRO-AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 95-134.
MEDLINE-91129241; PubMed-1993183;
Constantine K.L., Ramesh V., Banyai L., Trexler M., Patthy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDDINE-92114067; PubMed-1731074;
Constantine K.L., Madrid M., Banyai L., Trexler M., Patthy L.,
                                                                                                                           Braeuer C., Scheit K.H.; "Characterization of the gene for the bovine seminal vesicle "Characterization of the gene for the bovine seminal vesicle secretory protein SVSP109."; Biochim. Biophys. Acta 1090:259-260(1991).
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Braeuer C.C., Kleine Kuhlmann J.J., Hanes J.J., Scheit K.K.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biophys. Res. Commun. 113:861-867(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 26-134, AND DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE OF CARBOHYDRATE ON THR-36. MEDLINE=96234019; PubMed=8654577;
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                                                                             MEDLINE=92031704; PubMed=1932121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITE THR-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 350:203-206(1994).
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SEQUENCE FROM N.A.
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MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQD---DISSDEHPLFD-----KR 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jimenez B.C., Watkins M., Juszczak L.J., Cruz L.J., Olivera B.M.; "Contryphans from Conus textile venom ducts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                             SEMINAL PLASMA PROTEIN PDC-109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus textile (Cloth-of-gold cone).
Bukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                        Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          15480 MW; AD55FB8969B32224 CRC64;
                                                                                                                                                                                                                                       FIBRONECTIN TYPE-II, A. FIBRONECTIN TYPE-II, B. O-LINKED (GALNAC. . .).
/FTIG=CAR_000071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 QNCCNGGCSSKWC-----RDHARC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDCTVHGSLFPWCSLDADYVGRWKYCAQRDYAKC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Venom duct;
MEDLINE=21065889; PubMed=11137539;
                                                                                                                                                                                           PROSITE; PS00023; FIBRONECTIN_2; 2. Semen; Plasma; Glycoprotein; Repeat
                                                     -; NOT_ANNOTATED_CDS
                   EMBL; X60496; CAA43021.1; JOINED.
EMBL; X60497; CAA43021.1; JOINED.
EMBL; X60498; CAA43021.1; JOINED.
                                                                                                                                                            PRINTS; PR00013; ENTYPEII.
Prodom; PD000995; FN_TYPE_II; 2.
SMART; SM00059; FN2; 2.
PROSITE; PS00023; FIBRONECTIN_2;
                                                                                                                                           InterPro; IPR000562; FN_Type_II.
                                                    EMBL, X60960; -; NOT_ANNOTATED EMBL, Z33621; CA883915.1; -
PIR, A02256; WTBO.
PIR, A31852; A31852.
PIR, S18404; S18404.
PIR; S45010; S45010.
PBB; 1PDC; 31-JAN-94.
GlycoSulteDB; PQ2784; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.0%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contryphan-R/Tx precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxicon 39:803-808(2001).
AAA30766.1;
            CAA43021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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86
1119
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134 AA;
                                                                                                                                                     Pfam; PF00040; fn2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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49
94
36
 M22244;
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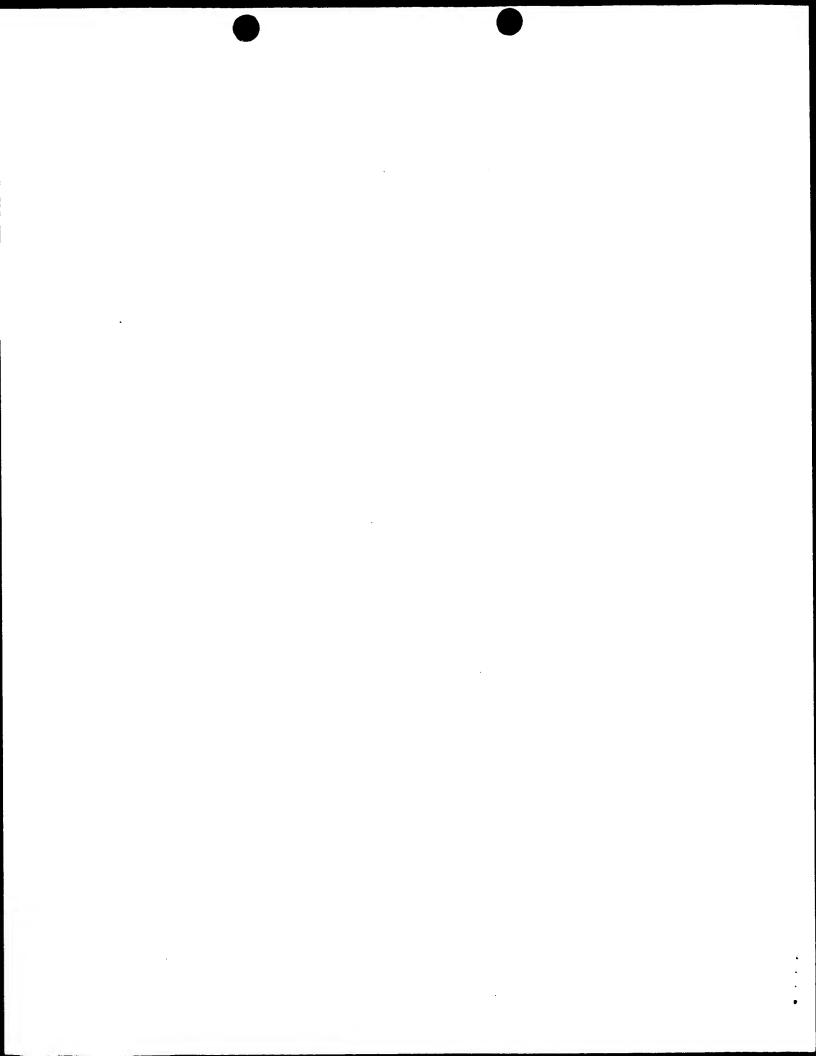
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                                                                                                                                                                                                                                                            CONTRYPHAN-R/TX (BY SIMILARITY).
PYROXYLATION (BY SIMILARITY).
D-AMIDATION (G-63 PROVIDE AMIDE GROUP) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                               5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        4 MSKLGVLLTVCLLLFPLTALPL-DGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             '2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                             Score 62.5; DB 1; Length 63; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: CONPAINS 2 KH DOMAINS.
                                                                                                                                                                                                             D-amino acid; Amidation; Signal
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
                                                                                                                                                                                                                                                                                                                            SIMILARITY).
9CB3C2C4796CFFE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C0664.1 in chromosome III.
                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                            EMBL; AF166325; AAF82245.1; -.
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Matches 20; Conserv
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P34307;
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15-JUN-2002
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YKR1_CAEEL
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Search completed: January 10, 2003, 08:32:57

Job time : 14.3913 secs

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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                    EA8EA91BB3AACD29 CRC64;
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33.3%; Pred. No. 27;
tive 9; Mismatches
                                                                                                                                                                                                                                             SMART; SM00322; KH; 3.
PROSITE; PS50004; KH_TYPE_1; 2.
Hypothetical protein; Repeat; RNA-binding.
DOMAIN 698 761
KH 1.
                                                                                                                                                                       WormPep; C06G4.1; CE28203.
InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH-domain; 2.
                                                                                                                                                                                                                                                                                                                                  103579 MW;
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Matches 17; Conservative
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January 10, 2003, 08:32:32; Search time 45 Seconds (without alignments) 343.412 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                           671580 seqs, 206047115 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_luman:*
5: sp_invertebrate:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*

5: 7: 10: 111: 112: 113: 114: 115: 116:

SUMMARIES

Result . 9

09bpj2 conus v 09bpj5 conus t 09bpj7 conus t 09bpj8 conus a Description 09bpj3 09bpj9 09bh61 O9bpj4 O9bpj6 O9bpk0 O9bpk0 098PJ5 098PJ7 098PJ1 098PJ3 098PJ3 098PJ4 098PJ4 098PJ4 098PJ4 098PJ4 098PJ4 **09BPJ2** Query Match Length DB 68 68 71 71 70 70 68 67 67 67 70.8 559.0 559.0 559.0 559.2 550.7 550.7 550.7 550.7 550.7 560.7 570.7 5 Score 297.5 263 263.5 251.5 251.5 242.5 242.5 236.5 236.5 237.5 217.5 217.5 217.5 219.5 219.5 219.5

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	5 098P94 5 098P31 5 098P13 5 098P19 5 098P18 5 098P10 5 098P5 5 098P13 5 098P13	10100	
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	22222222222222222222222222222222222222		64 15.2 64 15.2 .5 15.1 .5 15.1
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ALIGNMENTS

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		poda;			эчу 2.,	f Conop		Length 67; Indels	OKRONCC	H : H				
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67 AA.	updat on upd	Caeno			-Asher	: The	EE29 C	Score 297.5; DB 5; Pred. No. 9.8e-29; ; Mismatches 8;	ISSIGGO	ODDISS				AA.
67	notati	ne). opoda;	onus.		., Ben	bility	446546	297.5; No. 9. matche	RPAERM	FIIII RPAERM				72
PRT;	Created) Last sequence update) Last annotation update)	Conboxin scaticold III/IV. Conus ventricosus (Mediterranean cone). Eukaryota: Metazoa: Mollusca: Gastropoda; Caenogastropoda;	Neogastropoda; Conoidea; Conidae; Conus. NCBI_TaxID=117992; [1]	8371:	Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.;	"Mechanisms for Evolving Hypervariability: The Case of Conopeptides."; Mol. Biol. Evol. 18:120-131/2001.	932; AAG60360.1; 67 AA; 7399 MW; 04A221446546EE29 CRC64;	Score 297.5; DB 5 Pred. No. 9.8e-29; 5; Mismatches 8	MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCS	MMSKLGALLITCLLLFPLTALPLDGDQPADRPARRMQDDISSEQHPLFDKERQCCTGSCL				PRT;
::		IV. terrar lusca;	t; Conj	SEQUENCE FROM N.A. MEDLINE=21105969; PubMed=11158371;	Y., Av	19 Hype	0.1; MW;	38;	TALPLE	TALPLD				
· PRELIMINARY;	(TrEMBLrel. 17, (TrEMBLrel. 17, (TremBlrel. 19,	Conotoxin scatfold III/IV. Conus ventricosus (Mediter Eukaryota; Metazoa; Mollus	noidea ;	 PubMe	Gilad	volvin 18:120	EMBL; AF214932; AAG60360.1; SEQUENCE 67 AA; 7399 MW;	/at	LLLFPL	LLLFPL	74	29		PRELIMINARY;
PRELI		cattol icosus Metazo	Neogastropoda; Con NCBI_TaxID=117992; [1]	SEQUENCE FROM N.A. MEDLINE=21105969;	S.G.,	for E	932; A 67 AA;	ilarit Conse	VLLTVC	ALLTIC	SKWCRDHARCCG	NCWPCCG		PRELI
2.5	01-JUN-2001 01-JUN-2001 01-DEC-2001	oxin s ventr yota;	stropo TaxID=	NCE FR NE=211	Conticello S.G. Fainzilber M.:	anisms Biol.	AF214 NCE	tch al Sim 54;	MSKLG	4MSKLG	SKWCRD	ACW		
09BPJ2	01-JU 01-JU 01-DE	Conot	Neoga NCBI	SEQUE	Conti	"Mecha	EMBL; AF	Query Match Best Local Similarity Matches 54; Conserv	3		63 8	61 N	LT 2 J5	Q9BPJ5
Q9BPJZ ID Q9	FE	OCS	R OC	RP RX	RA RA	RT RL	DR SQ	Ou Be Ma	Οy	qq	Οy	Ωþ	RESULT 09BPJ5	0.5

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09BPJ3
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Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF214926; AAG60354.1; -.
                                                                                                                                                        "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
"Mechanisms Evol. 18:120-131(2001).
EMBL: AF214928; AAG60356.1;
SEQUENCE 72 AA; 7820 MW; EE6B0CB65BB43320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 68;
                                                                                                                 SEQUENCE FROM N.A.
MEDILINE-21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Painzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21105969; PubMed-11158371;
Conticello S.G., Gllad Y., Avidan N., Ben-Asher E., Levy Z.
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conotoxin scaffold III/IV.
Conus textile (Cloth-of-gold cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                        62.6%; Score 263; DB 5; Length 72; 66.2%; Pred. No. 1.6e-24; tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.9%; Score 251.5; DB 5; Length 66.2%; Pred. No. 3.8e-23; Live 8; Mismatches 11; Indels
                                  Conctoxin scaffold III/IV.

Conus textile (Cloth-of-gold cone).

Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;

Neogastropoda; Conoidea; Conidae; Conus.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
              01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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     01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                    61 VACNMGCEP-----CCG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7603 MW;
                                                                                                                                                                                                                                                                                                                             57 -- CNGGCSSKWCRDHARCCG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                          Best Local Similarity 66.2
Matches 53; Conservative
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Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF214933; AAG60361.1;
SEQUENCE 67 AA; 7364 MW; EF18D7A9F4ECAEE5 CRC64;
                                                                                                                                                                                                               "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."; Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF214925; AAG60353.1; SEQUENCE 68 AA; 7638 MW; 5D3B27B506B56828 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Gaps
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Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
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Conus textile (Cloth-of-gold cone).

Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;

Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-21105969; PubMed-11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
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Conus textile (Cloth-of-gold cone).
Eukaryota: Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                          Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=89451;
                                                                                                                                                                                                                                                                                                                                      59.8%; Score 251; DB 5; Length 68; 75.0%; Pred. No. 4.4e-23; Live 8; Mismatches 7; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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19, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
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Conotoxin scaffold III/IV. Conus arenatus (Sand-dusted cone).
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68.1%;
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Best Local Similarity 75.0°
Matches 45; Conservative
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Matches 49; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                          Fainzilber M.;
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                                   "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."; Mol. Biol. Evol. 18:120-131(2001).
EMBL: AF214930; AAG60358.1; -.
SEQUENCE 71 AA; 7836 MW; 1A4ACC90E6551360 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
Mol. Biol. Evol. 18:120-131(2001)
EMBL; AF214924, AAG60352.1:
InterPro: IPR001330; Prenyl_site.
PROSITE; PS00294; PRENYLAFION; DNKNOWN_1.
SEQUENCE 68 AA; 7526 MW; C6C4B30552DDC946 CRC64;
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                                                                                                                              Gaps
                                                                                                                                                             3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCN---- 58
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MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
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Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                   DB 5; Length 71;
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Neogastropoda; Conoidea; Conidae; Conus.
NCBL_TaxID=101317;
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Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=37335;
                                                                                                                           Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Conotoxin scaffold III/IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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                                                                                                 Match 57.7%; Score 242.5; DB 5 Local Similarity 61.5%; Pred. No. 4.9e-22; les 48; Conservative 6; Mismatches 9
                                                                                                                                                                                                                                                                                        68 AA.
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01-DEC-2001
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Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF214929; AAG60357.1; -.
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Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF214927; AAG60355.1; -.
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                                                                                                                                                                                                      3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNG--- 59
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MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
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Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus textile (Cloth-of-gold cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                55.7%; Score 234; DB 5; Length 70; 65.7%; Pred. No. 5.2e-21; ive 5; Mismatches 13; Indels
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Conus textile (Cloth-of-gold cone).
Conus textile (Cloth-of-gold cone).
Conus textile (Cloth-of-gold cone).
Newaryota: Metazoa: Mollusca; Gastropoda;
Newgastropoda; Conoidea; Conidae; Conus.
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                                                     70 AA; 7770 MW; 8A90EEDF3F90B301 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pred. No. 1.9e-19;
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01-JUN-2001 (TrEMBLrel, 17, Last seq
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50.5%;
EMBL; AF215094; AAG60515.1;
EMBL; AF214931; AAG60359.1;
SEQUENCE 70 AA; 7770 MW;
                                                                                                                           Best Local Similarity 65.7
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                         60 ---GCSSKWC
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SEQUENCE
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                                                                                            RESULT 13
Q9BPI6
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EMBL; AF214940; AAG60368.1; -.
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Mol. Biol. Evol. 18:120-131(2001).
EMBL, AF214923, AAG60351.1;
InterPro: IPR001230; Prenyl_site.
PROSITE: PS00294; PRENYLATION, UNKNOWN_1.
SEQUENCE 68 AA; 7613 MW; E01C4202318BF9F9 CRC64;
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                          Gaps
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Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 68;
52.7%; Score 221.5; DB 5; Length 70; 60.3%; Pred. No. 1.7e-19; Live 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 213; DB 5; Length 67; Pred. No. 1.8e-18;
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=101317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                      51.8%; Score 217.5; DB 5; Length (68.3%; Pred. No. 5.1e-19; ive 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7593 MW; 1A65FBD58E8DD811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.7%; Score 213; DB Best Local Similarity 60.6%; Pred. No. 1.8e Matches 43; Conservative 8; Mismatches
                                                                                                                                                                               68 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neogastropoda; Conoidea; Conidae; Conus
                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                               PRT;
                                                                                                                                                                                          Q9BPK0;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2002 (TrEMBLrel. 20,
Conotoxin scaffold III/IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conotoxin scaffold III/IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                         44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                 PRELIMINARY;
                                                                                                 62 S-SKWCRDHARCC 73
                                                                                                                       61 SYSCW----PCC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 41; Conserva
      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=101317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus tessulatus.
                                                                                                                                                                                                                                                     Conus tessulatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BPI4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BPI4
                                                                                                                                                                                  Q9BPK0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                             Matches
                                                                                                                                                            RESULT 11
                                                                                                                                                                        Q9BPK0
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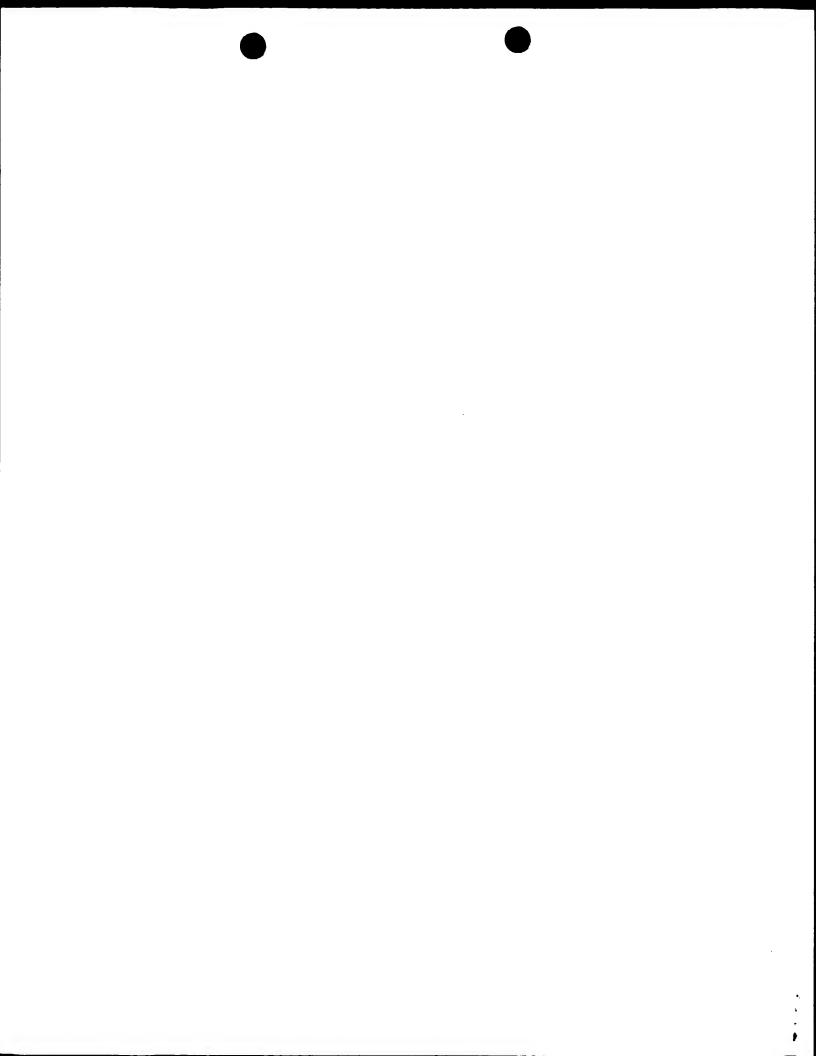
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Mol. Biol. Evol. 18:120-131(2001).
EMBL: AF214941; AAG60369.1; -.
SEQUENCE 67 AA; 7486 MW; 20E8D0858FDDD16D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."; Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF214938; AAG60366.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 MMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21105969; PubMed=11158371; Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.8%; Score 205; DB 5; Length 67; 60.6%; Pred. No. 1.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=101317;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=101317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.5%; Score 208; DB 5; Length 67, 62.0%; Pred. No. 7.2e-18;
Live 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 AA; 7502 MW; 20E8D096AEEFD16D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Conotoxin scaffold III/IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 AA.
                                                                                                                                                                                                                                                       67 AA.
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                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 SKWCRDHARCC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 SRYCYICIPCC 65
                                                                                              63 SKWCRDHARCC 73
                                                                                                                                        SRYCWKCIPCC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus tessulatus.
                                                                                                                                                                                                                                                                                                                                                                                             Conus tessulatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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63 SKWCRDHARCC 73

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Search completed: January 10, 2003, 08:37:35 Job time : 46 secs



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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 10, 2003, 08:32:32 ; Search time 22.1739 Seconds (without alignments) 99.519 Million cell updates/sec Run on:

US-09-910-009A-210 Perfect score:

1 GSMMSKLGVLLTVCLLLFPL.....CCNGGCSSKWCRDHARCCGR 75 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_AA:* Database :

/cgn2_6/ptodata/1/iaa/6A_COMB.pep:* /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* /cgn2_6/ptodata/1/iaa/backfiles1.pep:* /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 11, Appl	24,	, 6	9	37,		37,	39,		39,	37,	39,		Sequence 31, Appl	22,	22,		14,	7, 7	16,	16,	33,	37,	13,	3, 4	'n	3,
SUMMARIES	ID	US-07-689-693B-11	US-07-689-693B-24	-08-700-442A	-831-	-137-800	-08-137-	-477-	-477	-487-174	-487-174	US-08-480-750-37	US-08-480-750-39	5223423-3	US-09-488-799-31	US-09-061-026-22	US-09-466-138-22	US-09-061-026-14	US-09-466-138-14	US-08-599-556-7	-09-061-026	09-466-138	09-488	US-09-488-799-37	US-07-689-693B-13	-70	US-08-457-552-3	US-08-456-430-3
	DB	Н	-	7	4	П	1	-	-	Н	Н	Н	Н	9	4	m	4	m	4	Ţ	m	4	4	4	-	Н		-
	Length	89	52	333	333	64	64	64	64	64	64	64	64	3025	29	63	63	63	63	27	63	63	29	59	64	206	206	206
фp	Query	53.2	45.5	17.4	•	17.3		17.3		٠	•	17.3		17.3	17.0	17.0	17.0	16.8	16.8	16.7	16.3	16.3	15.6	15.6	15.6	15.6	15.6	15.6
	Score	223.5	191	73	73	72.5	72.5	72.5	72.5	72.5								70.5	70.5								65.5	
	Result No.	н	7	e	4	2	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

ALIGNMENTS

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NAME/KEY: textile
IDENTIFICATION METHOD: Libraries were created
IDENTIFICATION METHOD: using oligo-dT primed pUC13 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Prepropeptide sequence for three loop NAME/KEY: conotoxin from Circler conotoxin from Conus
                                                                                           GENERAL INCENTION:
APPLICANT: David Hillyard
APPLICANT: David Hillyard
APPLICANT: Baldomero M. Olivera
TITLE OF INVENTION: Segregated Folding Determinants
TITLE OF INVENTION: for Small Disulfide-Rich Peptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 5231011th & Western
STREET: 9035 South 700 East, Suite 200
                                                                                                                                                                                                                                                                                                                                                       STWAID.
COMDUTER RADABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: Compaq LTE/286
COMPUTER: Compaq LTE/286
COMPUTER: Compaq LTE/286
COMPUTER: Compag LTE/286
COMPUTER: Compag LTE/286
COMPUTER: OWG Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/689,693B
PTILING DATE: 19910418
                                              ; Sequence 11, Application US/07689693B
; Patent No. 5231011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Western, M. Wayne
REGISTRATION NUMBER: 22,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 566-6633
TELEFAX: (801) 566-0750
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: na ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
RESULT 1
US-07-689-693B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-689-693B-11
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                                           13; Gaps
                                                                                      4 MSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNC----CN 58
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0
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DB 1; Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.9%; Pred. No. 1.9e-14;
Matches 35; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Signal/Pro sequence for synthesis of NAME/KEY: three loop conotoxin from Circler conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 MSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFD 51
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                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: David Hillyard
APPLICANT: David Hillyard
APPLICANT: Baldomero M. Olivera
TITLE OF INVENTION: Segregated Folding Determinants
TITLE OF INVENTION: for Small Disulfide-Rich Peptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRI: .....
2.IP: 84070
COMPUTER 84070
COMPUTER COMPAGE DISKETCE, 3.5 inch, 720 Kb storage MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage COMPUTER: Compage LTE/286
COMPUTER: Compage LTE/286
COMPUTER: Compage LTE/286
COPRATING SYSTEM: DOS 4.01
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/689,693B
FILING DATE: 19910418
FILING DATE: 19910418
  53.2%; Score 223.5; DB 1 56.6%; Pred. No. 6.8e-18; tive 9; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Thorpe, No. 5231011th & Western STREET: 9035 South 700 East, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Western, M. Wayne
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: 9925
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 566-6633
TELEPAN: (801) 566-0750
INPORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                             RESULT 2
US-07-689-693B-24
; Sequence 24, Application US/07689693B
; Patent No. 5231011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19910418
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: na ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 amino acids
                                               Conservative
                                                                                                                                                                                                                           61 MGCKP-----CCG 68
                                                                                                                                                                                59 GGCSSKWCRDHARCCG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sandy
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US-08-700-442A-9
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                                                    43;
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                                                    Matches
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4 MSKLGVLLTVCLLLFPLTAL -----PLDGDQPADRPAE----RMQDDISSDEHPLFD 51
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APPLICANT: Shellen Frans BROEKAERT
APPLICANT: Willen Frans BROEKAERT
APPLICANT: Bupert William OSBORN
APPLICANT: Sarah Bronwen REES
APPLICANT: Ravindra Haribhai TAILOR
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS FROM ARALIA AND
TITLE OF INVENTION: IMPATIENS
                                                                                                    APPLICANT: Rupert William OSBORN
APPLICANT: John Anthony RAY
APPLICANT: Sarah Bronwen REES
APPLICANT: Ravindra Haribhai TAILOR
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS FROM ARALIA AND
TITLE OF INVENTION: IMPATIENS
CORRESPONDENCES: 21
CORRESPONDENCES: 22
CORRESPONDENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.4%; Score 73; DB 2; Length 333; 28.0%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Indels
                                                                                                                                                                                                                                                                   E: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,442A
FILING DATE: 19-AUG-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00509
FILING DATE: 09-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9404807.1
FILING DATE: 11-MAR-1994
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                           Sheila ATTENBOROUGH
Willem Frans BROEKAERT
Rupert William OSBORN
Sequence 9, Application US/08700442A Patent No. 5861480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08831028 Patent No. 6150588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.0°
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                         RY: USA
20005-3918
                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                        0.0
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                                                               APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                      STATE:
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17.4%; Score 73; DB 4; Length 333;
Best Local Similarity 28.0%; Pred. No. 1.2;
Matches 23; Conservative 13; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/700,442
FILING DATE: 19-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00509
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9404807.1
FILING DATE: 11-MAR-1994
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conotoxin Peptides
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,028
FILING DATE: 04-APP-1997
CLASSIFICATION BATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Olivera, Baldomero M. APPLICANT: Cruz, Lourdes J. APPLICANT: Hillyard, David R. APPLICANT: McIntosh, J. Michael APPLICANT: Santos, Ameurfina D. TITLE OF INVENTION: Conotoxin Pept NUMBER OF SEQUENCES: 53
                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/08137800 Patent No. 5514774 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 KRONCCNGGCSSKWCRDHARCC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: FIGURE 10
US-08-831-028-9
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             STREET: 1200
TTY: Richmond
                                                                                        USA
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--- 20005
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                                                                                        COUNTRY:
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9 VLLTVCLLLFPLTALPLDGDQPADRPAERMQD---DISSDEHPLFDKRQNCCNGGCSSKW 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                               17.3%; Score 72.5; DB 1; Length 64; 31.4%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches
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Patent No. 5514774
GENERAL INFORMATION:
APPLICANT: Olivera Baldomero M. APPLICANT: Cruz, Lourdes J.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: DC
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/137,800
FTLING DATE: 19-OCT-1993
                                                                                                       24260-104763
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                 CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2426(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 39:
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                    Conus striatus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 31.49
Matches 22; Conservative
                                                                                                                                                                                                                                   64 amino acids
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                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    amino acid
GY: linear
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 CRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Con
                                                                                                                                                                                                                                                    TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
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                                                                                                                            17.3%; Score 72.5; DB 1; Length 64; 31.4%; Pred. No. 0.25; tive 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24260-107673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameufino S.
TITLE OF INVENTION: Conotoxin Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRELIA AFELLIAN NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIPICATION: 435
PROPER APPLICATION 1835
PRICE APPLICATION BATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRICE APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/08477383 Patent No. 5589340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 24:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 37:
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                                                                                Conus striatus
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LENGTH: 64 amino acids
                                                                                                                                        Query Match 17.3%
Best Local Similarity 31.4%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear MOLECULE TYPE: peptide
peptide
NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            66 CRDHARCCGR 75
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                                        ANTI-SENSE: NO
CRIGINAL SOURCE:
CREANISM: Conu
US-08-137-800-39
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  MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-08-477-383-37
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                                       Gaps
                                                                         9 VLLTVCLLLFPLTALPLDGDQPADRPAERMQD---DISSDEHPLFDKRQNCCNGGCSSKW 65
                                                                                              13;
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 Length 64;
                                       24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
Ouery Match 17.3%; Score 72.5; DB 1; Best Local Similarity 31.4%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches
                                       11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conotoxin Peptides
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APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION UNBER: US 08/084,848
APPLICATION UNBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Machinosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptinumber OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      Sequence 39, Application US/08477383 Patent No. 5589340 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 31.4%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                                                                                          66 CRDHARCCGR 75
                                                                                                                                                                                               61 ----SCGR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM:
US-08-477-383-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                          US-08-477-383-39
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                                             22;
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                                             Matches
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24; Indels 13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN 1995
CLASSIFICATION: 514
                                                                                                                                                                                                           APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24260-107673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-UUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  Sequence 37, Application US/08487174 Patent No. 5595972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Thnen, Jeffrey L. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 24. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 37:
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Best Local Similarity 31.4%
Matches 22; Conservative
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LENGTH: 64 amino acids
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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66 CRDHARCCGR 75
                                        61 -----SCGR 64
                                                                                                                                                                                         GENERAL INFORMATION:
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ZIP: 20005
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                                                                                                                            US-08-487-174-37
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13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
17.3%; Score 72.5; DB 1; Length 64;
Best Local Similarity 31.4%; Pred. No. 0.25;
Matches 22; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                            ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIERCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Thnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMULICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                  Conotoxin Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/08A 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Pep
                  Sequence 39, Application US/08487174 Patent No. 5595972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/08480750; Patent No. 5633347; GENERAL INFORMATION:
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
                                                                                 APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEO ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
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ORGANISM: Conus striatus
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          Washington
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                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 20005
US-08-487-174-39
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RESULT 10

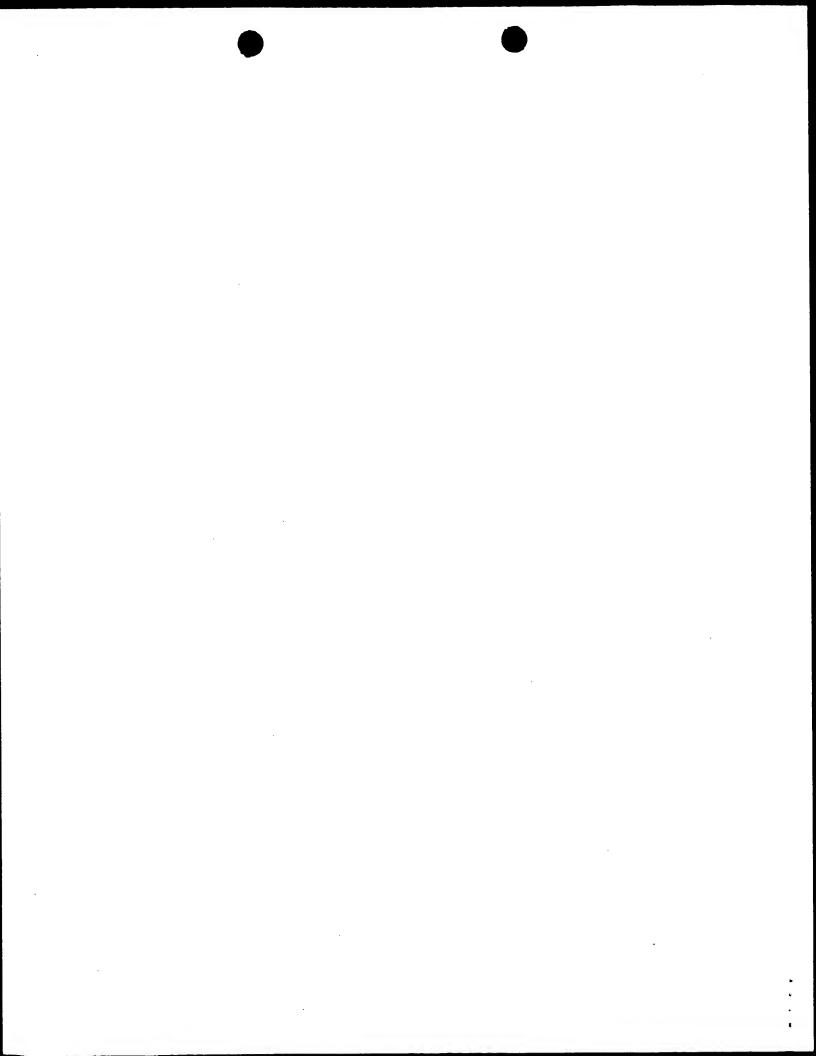
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ch 17.3%; Score 72.5; DB 1; Length 64; 1 Similarity 31.4%; Pred. No. 0.25; 22; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; APPLICANT: FRANCHINI, GENOVEFFA; WONG-STAAL, FLOSSIE; GALLO, ROBERT
                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,750 FILING DATE: US/01N11995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 03-31-1989
SEQ ID NO:3:
LENGTH: 3025
                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus striatus
                                                                                                   Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 22; Conserv
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Best Local Similarity
Matches 22; Conservi
                                                                                                                                            OPERATING SYSTEM:
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Washington
                                         U.S.A.
                                                                                                                                                                                                                                FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Patent No. 5223423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
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                                                           20005
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                                                                                                                             COMPUTER:
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                                         COUNTRY:
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5223423-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.3%; Score 72.5; DB 1; Length 64; 31.4%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                              E: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Datem: PC-DoS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFTCATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEPAX: 202-962-4810
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-480-750-39
US-08-480-750-39
Sequence 39, Application US/08480750
Sequence 39, Application US/08480750
Sequence 39, Application US/08480750
Septence 39, Application Olivera, Baldomero M. APPLICANT: Olivera, Baldomero M. APPLICANT: Hillyard, David R. APPLICANT: Maintosh, J. Michael APPLICANT: Santos, Ameurfino S. TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
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           APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA: RAPPLICATION DATA: US 08/084,848
APPLICATION NUMBER: US 08/084,848
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Conus striatus US-08-480-750-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                CORRESPONDENCE ADDRESS:
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hes 22; Conserva
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                                                                                                                                                                  Washington
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                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                        :: || ||: |:: || ||: ||: ||: ||: ||:: ||| ||::: ||| ||::: ||: ||: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||: ||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: 
24; Indels 13;
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10 LLTVCLLLFPLTALPLDGDQPADRPAERMQD---DISSDEHPLFDKRQNCCNGGCSSKWC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.0%; Score 71.5; DB 4; Length 59; Best Local Similarity 31.9%; Pred. No. 0.3; Matches 22; Conservative 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Baldomero M.
TITLE OF INVENTION: Contryphan Peptides
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
STREET: 755 Thirteenth Street N.W., Suite 701-E
CITY: Mashington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Hallyard, David R.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Schoenfeld, Robert
APPLICANT: Schoenfeld, Robert
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Alpha Conotoxin Peptides
FILE REFERENCE: Alphas 1
CURRENT APPLICATION NUMBER: US/09/488,799
CURRENT APPLICATION NUMBER: 60/116,881
EARLIER APPLICATION NUMBER: 60/116,881
EARLIER APPLICATION NUMBER: 60/116,882
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
                                 1878 ILSQLYRPL----ETCNNKCFCKGCCFHCQLC 1905
47 -----HPLFDKRQNCCNGGCSSKWCRDHARCC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/061,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                       Sequence 31, Application US/09488799 Patent No. 6268473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09061026 Patent No. 6077934 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Conus striatus
US-09-488-799-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentI
                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 RDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 ----SCGR 59
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CLASSIFICATION:
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                                                                                                                      RESULT 14
US-09-488-799-31
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                                              qq
δy
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4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.0%; Score 71.5; DB 3; Length 63; 30.8%; Pred. No. 0.32; tive 6; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: January 10, 2003, 08:38:16
Job time : 23.1739 secs
APPLICATION NUMBER: US 60/068,737 FILING DATE: 24-DEC-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                         2314-133
                                                             NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 JM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 GKFMNVLRRSGCPWEPWC 62
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 30.84
Matches 24; Conservative
                                                                                                                                                                                                                             63 amino acids
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-061-026-22
                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qý
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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January 10, 2003, 08:32:27; Search time 26.2609 Seconds (without alignments) 101.482 Million cell updates/sec Run on:

US-09-910-009A-211

121 1 XNCCNGGCSSKXCRDHARCC 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT: |
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT: |
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT: |
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT: |
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT: |
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT: |
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT: | /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980. /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982. /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1983. A_Geneseq_101002:* 14: 115: 116: 119: 220: 23:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	C striatus mu-cono	C striatus mu-cono	C striatus mu-cono	Cstercusmuscarum	Csterousmuscarum	C stercusmuscarum	C CODSOLS MU-CODOD	C consors mu-conop	C consors mu-conop	C bullatus mu-cono
ID	ABB88284	ABB88449	ABB88283	ABB88345	ABB88490	ABB88344	ABB88395	ABB88491	ABB88394	ABB88168
	23	23	23	23	23	23	23	23	23	23
% Query Match Length DB	20	20	75	22	22	97	22	22	74	26
% Query Match	97.5	96.7	96.7	78.5	77.7	7.7	60.3	59.5	59.5	58.7
Score	118	117	117	95	94	94	73	72	72	7.1
Result No.	1	7	3	4	2	9	7	8	σ	10

C bullatus mu-cono Human wound healin Human wound healin Human wound healin Human wound c tulipa mu-conope Human polypeptide	Propionibacterium C aurisiacus mu-co C nobilis mu-conop C stercusmuscarum C aurisiacus mu-co C stercusmuscarum
ABB88164 ABB88167 ABB88167 ABB88167 ABB88166 ABB88166 ABB88162 ABB88162 ABB88162 ABB88162 ABB88162 ABB88163 ABB88139 ABB88139 ABB88139 ABB88139 AANU07343 ABB88334 AANU07343 AANU79404	2 AAU54875 3 ABB88150 3 ABB88262 3 ABB88218 3 ABB88321 3 ABB88507 4 ABB88526 4 ABB88526 5 ABB88532
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ALIGNMENTS

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Location/Qualifiers
         ABB88284 standard; Peptide; 20 AA
                                       C striatus mu-conopeptide S3-2.
                            (first entry)
                                                                                                         Misc-difference 12
                                                                                           Misc-difference 1
                                                                            Conus striatus.
                            24-MAY-2002
                   ABB88284;
RESULT 1
     ABB88284
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Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder. /label= Gln, OTHER /note= "OTHER=pyroGlu" /label= Trp, OTHER /note= "bromo-Trp"

WO200207678-A2

31-JAN-2002

23-JUL-2001; 2001WO-US23125.

21-JUL-2000; 2000US-219619P.

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qq
δλ
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                                                                                                                                                                                                        The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, towning, suffocation, perinatal as physia, or hypoglycamenic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystenia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                 New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                              Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                              Watkins M, Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                         97.5%; Score 118; DB 23; 100.0%; Pred. No. 6.5e-07;
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                                                                                          Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C striatus mu-conopeptide SEQ ID NO: 432.
                                                                                 Garrett JE,
                                                                                          Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑA
                                                                                                                                                                                                                                                                                                                                                                                             97,77,
100.08; PIX
                                                                                                                                                                                           Claim 1; Page 56; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB88449 standard; Peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-219619P.
2000US-245157P.
2001US-264319P.
2001US-277270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2001; 2001WO-US23125
   2000US-245157P.
2001US-264319P.
2001US-277270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NCCNGGCSSKXCRDHARCC 20
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                                                 UTAH RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 19; Conservative
                                                                                              Jones RM,
                                                                                  Mcintosh
                                                           (COGN-) COGNETIX INC
                                                                                                                 WPI; 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                       20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus striatus
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03-NOV-2000;
29-JAN-2001;
21-MAR-2001;
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                                                   (UTAH ) UNIV
        03-NOV-2000;
                 29-JAN-2001;
21-MAR-2001;
                                                                                   Olivera BM,
                                                                                              Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB88449;
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
ABB88449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromusular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                      Shon K;
                                                                                                                                                                                            New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and neuroprotective agents
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                                                                            Cruz LJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                            Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.7%; Score 117; DB 23; 94.7%; Pred. No. 8.3e-07; 1ive 0; Mismatches 1;
                                                                                                       Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C striatus mu-conopeptide S3-2 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcintosh JM, Garrett JE,
                                                                                 Garrett JE,
                                                                                                          Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB88283 standard; Protein; 75 AA.
                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 85; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-245157P.
2001US-264319P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUL-2001; 2001WO-US23125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCCNGGCSSKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 NCCNGGCSSKXCRDHARCC 20
UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                               Mcintosh JM,
Jones RM, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COGNETIX INC
                                   COGN-) COGNETIX INC
                                                                                                                                                              WPI; 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus striatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200207678-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
                                                                                                             В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                       Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB88283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-)
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                                                                                                               Jacobsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB88283
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                                                                                                                                              which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amountophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, post-herpetic neuralgia, neurobaxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, perhatal as phyxia, or hypodyroamic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence
                                                       New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                       The present invention relates to mu-conopeptides derived from snails,
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                            96.7%; Score 117; DB 23; Length 75; 94.7%; Pred. No. 2.4e-06; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                 is a mu-conopeptide preprotein of the invention.
Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "OTHER=bromo-Trp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C stercusmuscarum mu-conopeptide Sm3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "OTHER=pyroGlu"
Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Trp, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Gln, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB88345 standard; Peptide; 22 AA.
                                                                                                                Claim 9; Page 56; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-219619P.
2000US-245157P.
2001US-264319P.
2001US-277270P.
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                                                                                                                                                                                                                                                                                                                                                                             NCCNGGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                     Conservative
Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus stercusmuscarum.
                       WPI; 2002-217020/27
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 14
                                                                                                                                                                                                                                                                                                       75 AA;
                                  N-PSDB; ABL88549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200207678-A2
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03-NOV-2000;
29-JAN-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 - MAY - 2002
 Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB88345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB88345
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                                                                                                                                                                                                                                                             voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mu-conopeptide; snail: venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiavascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                     Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                 mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                     Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.5%; Score 95; DB 23; Length 22; 80.0%; Pred. No. 0.00025; Live 2; Mismatches 0; Indels
                                                                                     Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C stercusmuscarum mu-conopeptide SEQ ID NO: 473.
                                                                                                                Shen GS;
                                                                                        Garrett JE,
                                                                                                                Cartier GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB88490 standard; Peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 69; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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2000US-245157P.
2001US-264319P.
2001US-277270P.
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(UTAH ) UNIV UTAH RES FOUND.
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                                                                                        Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                    Jones RM,
                                                                                                                                                                                                                                                                                                                          neuroprotective agents
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                                                                                                                                                                       WPI; 2002-217020/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200207678-A2.
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                                                                                        Olivera BM,
                                                                                                                       Jacobsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
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N-PSDB; ABL88578

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shon K;
   Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                          voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
blocking agents, as local anesthetic agents, as analgesic agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
                                                                                                                                                          New mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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   Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.7%; Score 94; DB 23; Length 22; 75.0%; Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stercusmuscarum mu-conopeptide Sm3-3 propeptide.
Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurodegenerative disease; neuromuscular disorder.

    Garrett JE, Watki
Cartier GE, Shen GS;

                                Shen GS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
   Ę,
   Garrett
                                Cartier GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB88344 standard; Protein; 76 AA.
                                                                                                                                                                                                                                                                                                                  Claim 1; Page 83; 231pp; English.
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29-JAN-2001; 2001US-264319P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CCNGRRGCSSRWCRDHSRCC
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Jones RM, C
   Mcintosh JM,
Jones RM, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
                                                                                                                                                                                                                                                        neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus stercusmuscarum
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                                                                                             WPI; 2002-217020/27
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 AA;
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Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2002
   Olivera BM,
Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
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                                                                                                                                                The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, post-herpetic neuropathy, ior reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypodlycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                         New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                       77.7%; Score 94; DB 23; Length 76; 75.0%; Pred. No. 0.00089; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "OTHER=hydroxy-Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Trp, OTHER
/note= "OTHER=bromo-Trp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB88395 standard; Peptide; 22 AA.
                                                                                                                      Claim 9; Page 69; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C consors mu-conopeptide Cn3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-245157P.
2001US-264319P.
2001US-277270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 CCNGRRGCSSRWCRDHSRCC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUL-2001; 2001WO-US23125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CCNG--GCSSKXCRDHARCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                     neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UTAH ) UNIV UTAH RES (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200207678-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus consors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000;
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29-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
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                                                                                                            voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiavascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
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             Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                              New mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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             Cruz LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
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             Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.071;
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    Garrett JE, Watki
Cartier GE, Shen GS;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C consors mu-conopeptide SEQ ID NO: 474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.3%; Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                         is a mu-conopeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB88491 standard; Peptide; 22 AA.
                                                                                                                                                                             Claim 1; Page 80; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CCN--GGCSSKXCRDHARCC 20
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2001US-264319P.
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               Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones RM,
                                Jones RM,
                                                                                                                                              neuroprotective agents
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                                                             WPI; 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
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Jacobsen R,
                              Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                       The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, post-herpetic neurodia, neuronal pain and phantom limb, burn pain, or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, trowning, suffocation, perinatal as physia, or hypodypacamic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
                                                              as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain: cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; asofropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shon K;
                                              voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mu-conopeptides useful for treating disorders associated with
                             mu-conopeptides useful for treating disorders associated with
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 23; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4, Garrett JE, Watki
Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.092;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C consors mu-conopeptide Cn3-3 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB88394 standard; Protein; 74 AA.
                                                                                                              Claim 1; Page 83; 231pp; English.
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2001US-264319P.
2001US-277270P.
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                                                                                                                                                                                                                                                                                                                                                                                                               59.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                               55.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                               neuroprotective agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COGNETIX INC
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WPI; 2002-217020/27.
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                                                                                                                                                                                                                                                                                                                                                                              22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2000;
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29-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
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ion channels. These may include neurodegenerative disorders such as severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, mycoradial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                                                                                           The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated
voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shon K;
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                               Score 72; DB 23; Length 74; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurodegenerative disease; neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "OTHER=bromo-Trp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB88168 standard; Peptide; 26 AA.
                                                             Claim 9; Page 80; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bullatus mu-conopeptide Bu3-3.
                                                                                                                                                                                                                                                                                                                                               59.5%;
55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                54 CCDVPNACSGRWCRDHAQCC 73
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2001US-264319P.
2001US-277270P.
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                                                                                                                                                                                                                                                                                                                                                                                                                3 CCN--GGCSSKXCRDHARCC
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones RM,
                               neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UTAH ) UNIV UTAH RE (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-217020/27.
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 18
                                                                                                                                                                                                                                                                                                                   74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200207678-A2.
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29-JAN-2001; 2
21-MAR-2001; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobsen R,
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB88168;
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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                                                                                                               The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, perilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mu-conopeptide, snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               58.7%; Score 71; DB 23; Length 26; 60.9%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.14; Mismatches
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/note= "OTHER=bromo-Trp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                      Claim 1; Page 29; 231pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bullatus mu-conopeptide Bu3-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CCN----GGCSSKXCRDHARCC 20
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03-NOV-2000; 2000US-245157P.
29-JAN-2001; 2001US-264319P.
21-MAR-2001; 2001US-277270P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                     neuroprotective agents
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 15
                                                                                                                                                                                                                                                                                                                                                                 26 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB88164;
                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                    voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
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                             mu-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23; Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurodegenerative disease; neuromuscular disorder.
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Cartier GE, Shen GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 70.5; DB Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a mu-conopeptide of the invention.
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                                                                                                                                                                                  Claim 1; Page 29; 231pp; English.
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2000US-245157P.
2001US-264319P.
2001US-277270P.
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65.0%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 AA;
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                                                         The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuroamscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroamscular and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypolycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease, neuromuscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shon K;
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                 DB 23; Length 26; 0.18;
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                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                 Score 70;
Pred. No. (
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Cartier GE, Sl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB88167 standard; Protein; 80 AA
                               Claim 1; Page 84; 231pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                    3 CCN----GGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                        5 CCNKGNGKRGC-SRWCRDHSRCC 26
                                                                                                                                                                                                                                                                                                                                 57.9%;
56.5%;
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2000US-245157P.
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neuroprotective agents
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                26 AA;
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29-JAN-2001;
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                                                                                                                                                                                                                                                                                                  Sequence
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amyotrophic lateral sclenosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuromuscular disorders, post-operative or spilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypodyzeamic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystohia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.
                 The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C bullatus mu-conopeptide SEQ ID NO: 493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB88510 standard; Peptide; 23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 CCNKGNGKRGC-SRWCRDHSRCC 77
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                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%;
56.5%;
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                    80 AA;
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                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
δy
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7

Gaps

9

2; Indels

Score 70; DB 23; Length 80;

Pred. No. 0.44; 2; Mismatches

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Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic; anaesthetic; neuromuscular blocking agent; neuroprotective; pain; cerebroprotective; anticonvulsant; antiaging; antidiabetic; cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine; neurodegenerative disease; neuromuscular disorder.
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03-NOV-2000; 2000US-245157P.
29-JAN-2001; 2001US-264319P.
21-MAR-2001; 2001US-277270P.
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(COGN-) COGNETIX INC
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Garrett JE, Watkins M, Shen GS; Cartier GE, Mcintosh JM, Jones RM, WPI; 2002-217020/27. Olivera BM, Jacobsen R,

Shon K;

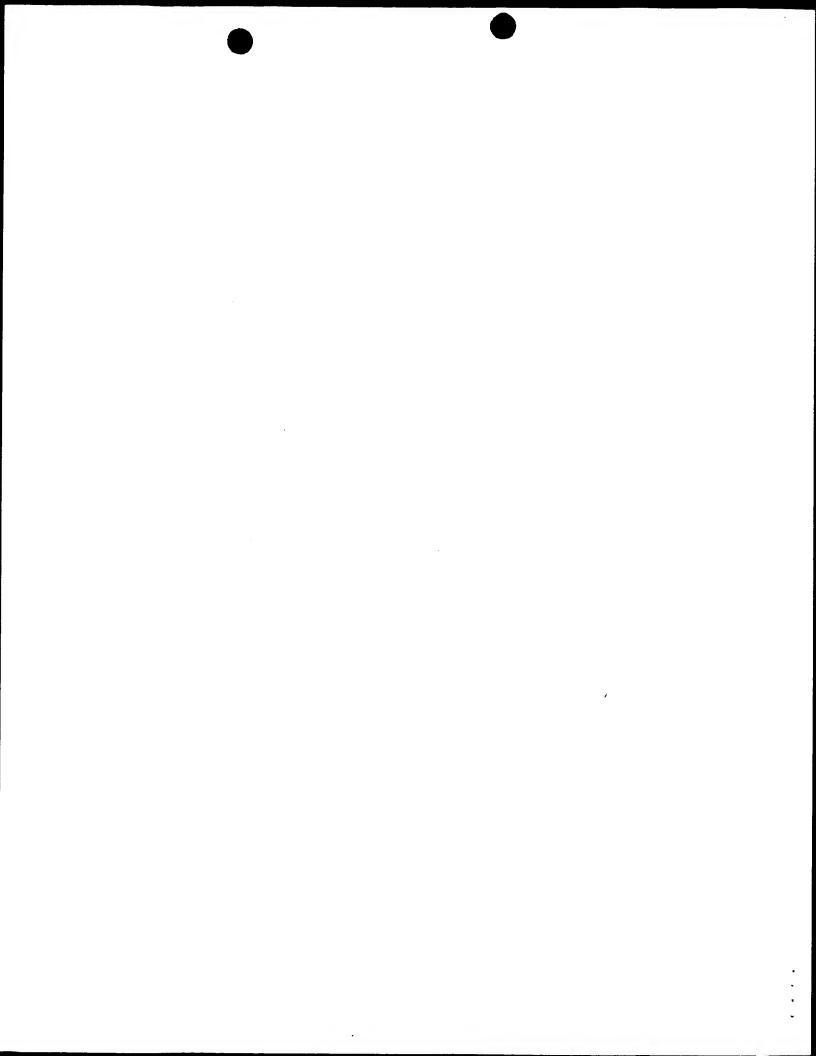
Cruz LJ,

voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as New mu-conopeptides useful for treating disorders associated with

neuroprotective agents

The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as Claim 1; Page 84; 231pp; English.

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amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
             servere chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neurolaia, neuronal pain and phantom limb, burn pain, pepilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal as phyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
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                                                                                                                                                                                                                                       DB 23; Length 23;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                     57.4%; Score 69.5; DB 60.0%; Pred. No. 0.18; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C bullatus mu-conopeptide Bu3-1A propeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB88163 standard; Protein; 77 AA.
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                                                                                                                                                                                                                                                                                                               CCNG--GCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                    CCKGKRGC-GRWCRDHSRCC 23
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2001US-264319P.
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nes 12; Conserv
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29-JAN-2001;
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                                                                                                                                                                                                     Sequence
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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January 10, 2003, 08:32:32; Search time 6.43478 Seconds Run on:

(without alignments) 298.796 Million cell updates/sec

US-09-910-009A-211 121 1 XNCCNGGCSSKXCRDHARCC 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		ultra-high-sulfur	nltra-bigh-sulfur	nline mign sarian	motellothionin t	hymothotical amoto	hypothetical prote	۲.	orvzain (EC 3.4.22	G profein-compled	metallothionein 20			- C		+	stanniocalcin prec	hypothetical prote			Sulfur r	hetica	+	proteoliaisin - se	5	metallothionein 10		granulin precursor	Omega-conotoxin MV	
SUMMARIES		B38346	A38346	S18946	A34484	H86231	T49670	T46722	KHRZOB	S40241	S47576	S39420	S39421	T18975	T24272	T01206	A54648	T25933	E36787	S38929	JC6547	T15651	S24602	T30274	S39416	S39419	S39417	GYHU	A58537	A34905
DB	1	7	7	Н	7	~	~	7	Н	7	7	7	7	7	7	7	7	~	7	7	7	7	7	7	7	7	~	Н	7	7
Length		223	230	169	63	454	147	389	471	1115	7.1	7.1	71	152	164	493	263	1372	82	87	188	188	464	1297	72	72	72	593	29	63
% Query Match		43.8	43.8	43.0	42.6	•	41.7	41.3	41.3	40.5	40.1	40.1	40.1	40.1	40.1	40.1	39.7	39.7	38.8	38.8	38.8	38.8	38.8	38.8	38.4	38.4	38.4	•	38.0	38.0
Score		53	53	52	51.5	51	50.5	20	20	49		φ,	ж •	8	æ	48.5	48	48	47	47	47	47	47	4		ė.	46.5			46
Result No.		~ +	7	ĸ	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

hypothetical prote cellular nucleic a	zinc finger protei cellular nucleic a	cellular nucleic a	ornithine decarbox	Cysteine proteinas UL43 protein - hum Cysteine proteinas	probable zinc meta metallothionein 10	DELTA-like 1 - mou metallothiopein II	metallothionein II
T24715 I48297	A55499 I48298 A32760	JC2512 I49259	A55472	WMBEF3 T06416	T37819 S39418	148324 SMRT2	SMMS2
222	7 77 7	122	2 2	7 7	7 7	7	⊣
170	171	177	227	434	512 72	722	61
38.0	38.0	38.0	38.0	38.0	38.0	37.6	37.2
4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4	4 6	4 4 6 4	46	46 45.5	45.5	4 5
30 31	3 8 8 3 8 4	35 36	37 38	39	41	4 4 4 4	45

ALIGNMENTS

Н	
ч	B38346

ultra-high-sulfur keratin 2 - mouse

C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C; Accession: A38660, B38346
B; Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 266, 4024, 1991
A; Title: Serine-rich ultra high sulfur protein gene expression in murine hair and ski A; Reference number: A38660; MUID:91154184; PMID:1840598

A;Molecule type: DNA A;Residues: 1-223 <WO2> A;Cross_references: GB:M37760; NID:g200963; PIDN:AAA40107.1; PID:g200964

A;Note: this is a correction
R;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and ski
A;Reference number: A38346; MUID:91065960; PMID:2250030
A;Accession: B38346

A;Molecule type: DNA A;Residues: 1-21,'GGCGSGCGGCGSNCGGCGSSCCKPVCC',22-40,'GSS',44-45,'G',47-48,'S',50,'GS

A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962 A;Note: the sequence reported in this paper has been corrected. See A38660 C;Superfamily: ultra-high-sulfur keratin

Gaps 5; DB 2; Length 223; Indels 5; 43.8%; Score 53; DB 44.4%; Pred. No. 13; ative 3; Mismatches Query Match
Best Local Similarity 44.4
Matches 8; Conservative

3 CCNGGCSSKXCRDHARCC 20 ò

159 CCSSGCGSSCCQ--SSCC 174 QQ

ultra-high-sulfur keratin 1 - mouse C;Species: Mus musculus (house mouse) C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999 C;Accession: A38346 R;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G. J. Biol. Chem. 265, 21375-21380, 1990 A;Titler: Serine-rich ultra high sulfur protein gene expression in murine hair and ski A;Reference number: A38346; MUID:91065960; PMID:2250030

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <WOO>
A;Residues: 1-230 <WOO>
A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
C;Superfamily: ultra-high-sulfur keratin

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3 CCNGGCSSKXC---RDHARCC 20
                                                                                                                                                  42.6%;
                                                                                                                                                                                                                                                                      2 NCCNGGCSSKXCRDHARC 19
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                                                                                                                                                                                                                                                                                                                           15 NCANGGCQ---CGDKCEC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 NCCRGGVLTSMSQDHA 193
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Status: preliminary A, Molecule type: DNA
A; Residues: 1-63 <MEH>
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                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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A; Mostecule type: mRNA
A; Residues: 1-169 cDRA
A; Cross references: BMBL; X63755; NID:g32471; PIDN:CAA45283.1; PID:g32472
A; Cross references: BMBL; X63755; NID:g32471; PIDN:CAA45283.1; PID:g32472
B; MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.
J. Cell Biol. 111, 2587-2600, 1990
A; Title: Structure and expression of genes for a class of cysteine-rich proteins of the A; Reference number: A36686; MUID:91115951; PMID:1703541
A; Accession: B3686
A; Molecule type: DNA
A; Accession: B3686
A; Molecule type: DNA
A; Cross -references: GB:X55293; NID:g34078; PIDN:CAA39005.1; PID:g34079
A; Cross -references: GB:X55293; NID:g34078; PIDN:CAA39005.1; PID:g34079
A; Cross -references: GB:X55293; NID:ga4078; PIDN:CAA39005.1; PID:g34079
A; Cross -references: GB:X55293; NID:ga4078; PIDN:CAA39005.1; PID:g34079
C; Genetics:
A; Map position: 11q13-11q13
A; Cross -references: GB:X55293; NID:ga4078; PIDN:CAA39005.1; PID:g34079
C; Superfamily: ultra-high-sulfur keratin
C; Superfamily: ultra-high-sulfur repeat
F; 7-15/Region: Cys-rich decapeptide repeat
F; 79-88/Region: Cys-rich decapeptide repeat
F; 98-107/Region: Cys-rich decapeptide repeat
F; 108-1107/Region: Cys-rich decapeptide repeat
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C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C; Accession: A34484
R; Mehra, R.K.; Garey, J.R.; Butt, T.R.; Gray, W.R.; Winge, D.R.
J. Biol. Chem. 264, 19747-19753, 1989
A; Title: Candida glabrata metallothioneins. Cloning and sequence of the genes and charac
A; Reference number: A92737; MUID:90062075; PMID:2584191
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                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                             ultra high-sulfur keratin 1 - human N;Alternate names: UHS keratin; ultra high-sulfur matrix protein N;Alternate names: UHS keratin; ultra high-sulfur matrix protein C;Species: Homo sapiens (man) C;Decies: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 C;Accession: S18946 Bio686 Sibrabert, B.; Doenecke, Doenecke, B.; A;Persant, B.; Doenecke, B.; A;Persant, B.; Doenecke, B.; Description: Nucleotide sequence of a Human high-sulphur keratin cDNA. A;Reference number: S18946
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                                              Length 230;
                                                                                                          5; Indels
                                              5;
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                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F,127-136/Region: Cys-rich decapeptide repeat
F;137-145/Region: Serrich nonapeptide repeat
F;146-155/Region: Cys-rich decapeptide repeat
F;156-165/Region: Cys-rich decapeptide repeat
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                                              Score 53;
Pred. No.
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44.48;
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                                                                                                             Conservative
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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A; Molecule type: DNA
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hypothetical protein [imported] - Arabidopsis thaliana
c) Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: H66231
C; Accession: H66231
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Hughes, B.; Huizar, L.
Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J., Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.Authors: Hunter, J.L.; Jankins, J. Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallo A; Authors: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Reference number; A86141; MUID:21016719; PMID:11130712
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R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
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C;Genetics:
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C.Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
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                                                                                                                                                                                                        Gaps
A;Cross-references: GB:J05133; NID:g173321; PIDN:AAA35272.1; PID:g173322 A;Note: the authors translated the codon GAG for residue 61 as Asp C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
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A;Molecule type: DNA
A;Residues: 1-147 <SCH>
A;Cross-references: EMBL:AL355933; GSPDB:GN00116; NCSP:B8B20.240
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C;Superfamily: Neurospora crassa hypothetical protein B8B20.240
                                                                                                                                    Length 63;
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                                                                                                                                                                                                     Indels
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                                                                                                                                           5;
                                                                                                                                           Score 51.5; DB Pred. No. 8.7; 0; Mismatches
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Pred. No. 35;
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50.0%;
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C;Dates vorum: 240241
C;Accession: S40241
C;Accession: S40241
C;Accession: S40241
C;Accession: S40241
C;Baccesion: S40241
C;Baccesion: J.F.; Heerikhuizen, H.;
Submitted to the EMBL Data Library, June 1993
A;Description: A G protein-coupled receptor with LDL-binding motifs suggests a role f
A;Reference number: S40241
                                                                                                                                                                                                                                                                                                                                                                                       A)Cross-references: EMBL:223104; NID:9438128; PID:9438129
A)Cross-references: EMBL:223104; NID:9438128; PID:9438129
C)Superfamily: great pond snail LDL receptor-related G protein-coupled receptor; LDL
C)Keywords: G protein-coupled receptor; transmembrane protein
E):38-77/Domain: LDL receptor ligand-binding repeat homology <LDL1>
E;79-113/Domain: LDL receptor ligand-binding repeat homology <LDL2>
G protein-coupled receptor - great pond snail
C.Species: Lymnaea stagnalis (great pond snail)
C.bate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;233-267/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;234-267/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;274-316/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;367-401/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;367-401/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;446-483/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;486-53/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;884-607/Domain: LDL receptor ligand-binding repeat homology <LDR1>
F;884-607/Domain: LDL receptor ligand-binding repeat homology <LRR1>
F;686-631/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;632-655/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;704-727/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;774-797/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;774-797/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
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1; Mismatches 9; Indels
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A;Residues: 1-71 <AMAC>
C;Superfamily: metallothionein
C;Keywords: chelation: metal binding
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S47576
metallothionein 20-1b - blue mussel
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Best Local Similarity 44.4
Matches 8; Conservative
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Best Local Similarity 40.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1115 <TEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;118-153/Domain: LDL re
F;158-194/Domain: LDL re
F;158-230/Domain: LDL re
F;233-267/Domain: LDL re
F;234-316/Domain: LDL re
F;322-361/Domain: LDL re
F;367-401/Domain: LDL re
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A; Mesidues: 1.471 < WATI->

R; Wattanabe, H.; Abb, K.; Emori, Y.; Hosoyama, H.; Arai, S.

J. Biol. Chem. 266, 16897-16902, 1991

J. Biol. Chem. 266, 16897-16902, 1991

A; Title: Molecular cloning and gibberellin-induced expression of multiple cysteine prote

A; Reference number: A40053; MUID:91358494; PMID:1885617
                                                                                                                                                                                                                                                         C; Species: Leishmania major
C; Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C; Accession: T4672v
R; Volckaert, G; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                           conserved hypothetical protein [imported] - Leishmania major N;Alternate ananes: probable proline synthetase associated protein (:Species: Leishmania major (:Species: Leishmania major (:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryzáln (EC 3.4.22.-) beta precursor - rice
C;Species: Oryza sativa (rice)
C;Date: 31-Mar.1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
C;Accession: JU0389; B40053
R;Watanabe, H; Abe, K; Emori, Y; Hosoyama, H.; Arai, S.
submitted to JIPID, May 1991
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A; Cross-references: GB:D90407; NID:g218182; PIDN:BAA14403.1; PID:g218183
A; Cross-references: GB:D90407; NID:g218182; PIDN:BAA14403.1; PID:g218183
C; Superfamily: papain rectainse; glycoprotein; hydrolase; seed
C; Superfamily: papain sequence #status predicted <SIG>
F; 1-21/Domain: amino-terminal propeptide #status predicted <PRO>
F; 140-360/Product: oryzain beta #status predicted <ART>
F; 361-471/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F; 161-204, 195-237, 295-346/Disulfide bonds: #status predicted
F; 164, 301, 321/Active site: Cys, His, Asn #status predicted
F; 340, 388/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: T46722
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Mismatches
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain Friedlin C; Genetics:
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   30 CCHGPCSSRRAAPTSPRIRCC 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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Best Local Similarity
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Gaps

Length 1115;

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R; Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.<u>H.</u>R
                                                                                                                          Eur. J. Biochem. 218, 183-194, 1993
A,Title: Complete amino acid sequences of five dimeric and four monomeric forms
A,Reference number: S39416; MUID:94062828; PMID:8243463
                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $39420
metallothionein 20-Ia - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Species: Mytilus edulis (blue mussel)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 17-Mar-1999
C;Accession: S47576
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Pred. No. 21;
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Search completed: January 10, 2003, 08:36:22 Job time: 8.43478 secs
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C;Species: Mytilus edulis (blue mussel)
C;Oate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: 539421
R;Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; F
Eur. J. Blochem. 218, 183-194, 1993
A;Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal
A;Reference number: 539416; MUID:94062828; PMID:8243463
A;Accession: 53941
A;Accession: 539402
A;Anolecule type: protein
A;Residues: 1-71 <AMC>
C;Superfamily: metallothionein
C;Seywords: chelation; metal binding
C;Accession: S39420
R;Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; F
Eur. J. Biochem. 218, 183-194, 1993
A;Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal
A;Reference number: S39416; MUID:94062828; PMID:8243463
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Nypotherical protein C06Al.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
C;Accession: T18975
R;Mowntray, A.
Submitted to the EMBL Data Library, June 1995
A;Recession: T18975
A;Recession: T18975
A;Recession: T18975
A;Stctus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-152 <WIL>
A;Residues: 1-152 <WIL>
A;Cross-references: EMBL:249886; PIDN:CAA90055.1; GSPDB:GN00020; CESP:C06Al.6
A;Experimental source: clone C06Al
C;Genetics:
A;Gene: CESP:C06Al.6
A;Map position: 2
A;Introns: 22/3
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                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                        Query Match 40.1%; Score 48.5; Dest Local Similarity 40.7%; Pred. No. 21; Matches 11; Conservative 1; Mismatches
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                                                                                                                                          A;Molecule type: protein
A;Residues: 1-71 <MAC>
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding
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es 9; Conserv
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Best Local Similarity
Matches 11; Conserv
                                                                                                                     A; Accession: S39420
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Mypothetical protein T01B7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T24272
R;Sims, M.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z19867
A;Refere
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Pred. No. 36;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cysteine proteinase mir2 (EC 3.4.22.-) - maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 ccecegegegecccccrprccc 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CC---NGGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.1%;
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 2
A; Introns: 20/3; 90/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:T01B7.8
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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January 10, 2003, 08:32:27; Search time 3.30435 Seconds (without alignments) 251.041 Million cell updates/sec Run on:

Title: US-09-910-009A-211
Perfect score: 121
Sequence: 1 XNCCNGGCSSKXCRDHARCC 20

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	075690 homos applied		Candi	- ru	eduns	lymnae	⊐	mytilu	mytilus		P18301 anquilla au			Q9w6d8 qallus qall	ictalur		Q9c0a0 homo sapien	myti]	mytilus	mytilus	h qranul	8		P53996 mus musculu			_	P54370 rattus norv	P20721 lycopersico		-	8	8
SUMMARIES		KRUB_HUMAN	KRUA_HUMAN	MT1_CANGA	ORYB_ORYSA	MT1A_HORSE	GPCR_LYMST	CXM3_CONPU	MT21_MYTED	MT22_MYTED	CXO3_CONST	STC_ANGAU	FLIB_SALCH	FLIB_SALTY	BRX1_CHICK	VG13_HSVI1	OAZ_MESAU	CTA4_HUMAN	MT14_MYTED	MT1A_MYTED	MT1B_MYTED	GRN_HUMAN	CXOD_CONMA	MT2_CAEEL	CNBP_MOUSE	CNBP_CHICK	CNBP_HUMAN	OAZ_MOUSE	OAZ_RAT			YE94_SCHPO	DLL1_HUMAN	MT13_MYTED
	DB	;	Т	-	Н	٦	Н	Н	Н	-	-	-	Н	-	-	Н	-	-	Н	Н		П	J			Н	-		Н	Н	Н	Н	1	П
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Q9u568 perna virid	P97677 rattus norv	061483 mus musculu	P02799 cricetulus	P02798 musculu	P04355 rattus norv	O14508 homo sapien	PO4605 human immun	O14894 homo sapien	P54190 toxocara ca	P07981 trichoderma	Q12714 trichoderma
MT_PERVI	DLL1_RAT	DLL1_MOUSE	MT2_CRIGR	MT2 MOUSE	MT2_RAT	WFD2 HUMAN	TAT_HV2RO	T4S5 HUMAN	TE26_TOXCA	GUN1 TRIRE	GUN1_TRILO
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73	714	722	61	61	61	124	130	197	262	459	463
37.6	37.6	37.6	37.2	37.2	37.2	37.2	37.2	37.2	37.2	37.2	37.2
45.5	45.5	45.5	45	45	45	45	45	45	45	45	45
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

RESULT 2

KRUA_HUMAN

1;

2; Gaps

Query Match
43.8%; Score 53; DB 1; Length 194;
Best Local Similarity 44.4%; Pred. No. 2.3;
Matches 8; Conservative 3; Mismatches 5; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR KERATINS (40-56 kDa).
TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99148005; PubMed-10023043; Perez C., Auriol J., Gerst C., Bernard B.A., Egly J.-M.; Genomic organization and promoter characterization of two human UHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION. -!- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                  Keratin, ultra high-sulfur matrix protein A (UHS keratin A) (UHS
                                                                                                                                                                                                                                                                                 McKinnon P.J., Powell B.C., Rogers G.E.; "Structure and expression of genes for a class of cysteine-rich proteins of the cuticle layers of differentiating wool and hair follicles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 1; Length 169; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! - SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 148021; -.
Keratin; Repeat; Multigene family
                                                                                                                                                                                                                                                                                                                                                            Cell Biol. 111:2587-2600(1990).
                                                                                                                                                                                                                                                          FISSUE=Follicle;
MEDLINE=91115951; PubMed=1703541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ006693; CAA07189.1; -. HSSP; P01064; 1PI2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X55293; CAA39005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 CCSSGCGSSCCQ--CSCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CCNGGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:6409; KRN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 227:137-148(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RICH (SR) REPEATS.
                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAIR FOLLICLES.
                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             keratin genes."
                                                                                                                              KRN1 OR UHSK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MT1_CANGA
P15113;
 KRUA HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
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                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=90062075; PubMed=2584191;
MEDLINE=90062075; J.R., Butt T.R., Gray W.R., Winge D.R.;
Mehra R.K., Garey J.R., Butt T.R., Gray W.R., Winge D.R.;
"Candida glabrata metallothioneins. Cloning and sequence of the genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                       Mehra R.K., Tarbet B.E., Gray W.R., Winge D.R.;
"Metal-specific synthesis of two metallothioneins and gamma-glutamyl
peptides in Candida glabrata.";
Proc. Natl. Acad. Sci. U.S.A. 85:8815-8819(1988).
-!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
SEQUESTRATION OF TOXIC METAL IONS.
-!- INDUCTION: BOTH MT-I AND MT-II GENES ARE REGULATED BY COPPER ION
                                                                                                                                                                                                                                                                                                                                                                                               IN A CONCENTRATION-DEPENDENT FASHION, AND BOTH ARE INDUCIBLE BY SILVER BUT NOT BY CADMIUM SALTS.

-1- MISCELLANEOUS: MT-I MIGHT BIND APPROXIMATELY 11-12 MOL EQ OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta: Embryophyta; Tracheophyta;
                           Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51.5; DB 1; Length 62; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metal-binding; Metal-thiolate cluster; Copper; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-cv. Nipponbare; TISSUE-Seed;
MEDLINE-01358494; PubMed-1885617;
Watanabe H., Abe K., Emori Y., Hosoyama H., Arai S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80D768C06C44F7A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 471 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryzain beta chain precursor (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                          and characterization of proteins.";
J. Biol. Chem. 264:19747-19753(1989).
                                                                                                                                                                                                                                             SEQUENCE OF 1-16.
MEDLINE=89057829; PubMed=3194392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J05133; AAA35272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6243 MW;
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PIR; A34484; A34484.
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                                                                                                                       SEQUENCE FROM N.A.
Metallothionein-I.
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                                                                                    NCBL_TaxID=5478;
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P25777;
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NCBI_TaxID=6523;
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113
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P46023;
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METAL
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                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE (POTENTIAL).
ORYZAIN BETA CHAIN.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
"Molecular cloning and gibberellin-induced expression of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                 Length 471;
                                                                                                                                                                                                                                           PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
Hydrolase; Thiol protease; Zymogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                OBF39D33995CEB1D CRC64;
         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                    Interpro; IPR000118; Granulin.
Interpro; IPR000668; Peptidase Cl.
Interpro; IPR000169; Shprot_acsite.
Pfam; PF00112; Peptidase_Cl; 1.
Pfam; PF00396; granulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rends Biochem. Sci. 3:90-93(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISION TO 60, AND VARIANT ARG-39
                                                                                                                                                                                                                  PRINTS; PR00705; PAPAIN.
ProDom; PD000158; Peptidase_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               407 CLVWGCCPVEGATCCKDHASCC 428
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                                                                                                                                                                                                                                                                                                                                                                                 50505 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 41.3%;
                                                                                                                                    EMBL; D90407; BAA14403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CCNGGC----SSKXCRDHARCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metallothionein-IA (MT-1A).
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TISSUE=Liver, and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kojima Y., Kaegi J.H.R.; "Metallothionein.";
                                                                                                                                                                                                                                     SMART; SM00277; GRAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                  471
164
301
321
204
237
                                                                                                                                            PIR; JU0389; KHRZOB.
HSSP; P00785; ZACT.
                                                                                                                                                                                                                                                                                                                                                                               471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                              MEROPS; C01.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9796;
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P02800;
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                                                                                                                                                                                                                                                                                                          ACT_SITE
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                                                                                                                                                                                                                                                                                                   CHAIN
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-!- SUBUNIT: MONOMER.
-!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
-!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
-!- FOUR DIVALENT IONS ARE CHELATED WITHIN CLISTERS A OF THE ALPHA
DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CYSTEINE LIGANDS. CLIGGTER B, THE CORRESPONDING REGION WITHIN THE
BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, East annotation update)
15-Minaea stagnalis (Great pond snail)
Eukaryota; Metazoa; Mollusca: Gastropoda; Pulmonata; Basommatophora;
Kaegi J.H.R., Kojima Y.;
"Chemistry and biochemistry of metallothionein.";
Experientia Suppl. 52:25-61(1987).
-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00131; metalthio; 1.
PRINTS; PR00860; MTVERTEBRATE.
PROSTE; PS00203; MATALLOTHIONEIN_VRT; 1.
Metal-binding; Metal-thiolate cluster; Acetylation.
DOMAIN 1 29 BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1115 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA.
CLUSTER E
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                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003019; Metallthion.
InterPro; IPR00006; Metllthion_vert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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48
48
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57
59
60
                                                                                                                                                                                                                                                                                                            PIR; A03277; SMHOlA.
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                                                                                                                                  GLUCOCORTICOIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                   HSSP; P02795; 1MHU
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us-09-910-009a-211.rsp

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MEDLINE=94255418; PubMed=8197140;
Tensen C.P., van Kesteren E.R., Planta R.J., Cox K.J.A., Burke J.F., van Heerikhuizen H., Vreugdenhil E.;
A G protein-coupled receptor with low density lipoprotein-binding motifs suggests a role for lipoproteins in G-linked signal transduction.";
Proc. Natl. Acad. Sci. U.S.A. 91:4816-4820(1994).
-!- FUNCTION: MIGHT DIRECTLY TRANSDUCE SIGNALS CARRIED BY LARGE EXTRACELULAR (LAPO) PROTEIN(COMPLEXE)S INTO NEURONAL EVENTS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN A SMALL NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 221104; CAA86651.1; -.

REMBL; 221104; CAA86651.1; -.

RISPY Q07954, 1CRB.

RICTORD; IPR002175; GPCR_Rhodpsn.

InterPro; IPR002172; LDL_recept_A.

InterPro; IPR003172; LDL_recept_A.

InterPro; IPR003591; LRR_Ltyp.

RICTORD; IPR003591; LRR_Ltyp.

RICTORD; IPR003591; LRR_Ltyp.

REMIN; PF000601; 7Lm_1; 1.

REMIN; PR00560; LRR; 6.

REMIN; PR00560; LRR; 6.

REMIN; PR00237; GPCRRHOOPSN.

REMINS; PR00261; LDLRECEPTOR.

REMART; SM00013; LDLRECEPTOR.

REMART; SM00013; LDLRR; 1.

REMART; SM00014; LDLRR; 1.

REMART; SM00015; LDLRR; 1.

REMART; SM000169; LDLRA; 1.

REMART; SM000169; LDLRA; 1.

REMART; SM00169; LDLRA; 1.

REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART; REMART;
                                                                                                                                                                                                                                                NEURONS WITHIN THE CENTRAL NERVOUS SYSTEM AND TO A LESSER EXTENT IN THE HEART.
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12 X 40 AA APPROXIMATE TANDEM REPEATS
SIMILAR TO THE LDL-RECEPTOR CLASS A.
                                                                                                                                                                                                                                                                                           - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS:
- SIMILARITY: CONTAINS 12 LDL RECEPTOR CLASS A DOMAINS.
- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
G-PROTEIN COUPLED RECEPTOR GRL101.
EXTRACELLULAR (POTENTIAL).
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7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
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(POTENTIAL).
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LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 10.
LDL-RECEPTOR CLASS A 10.
LDL-RECEPTOR CLASS A 10.
LDL-RECEPTOR CLASS A 11.
LRR 1.
LRR 2.
LRR 3.
LRR 3.
LRR 5.
LRR 6.
LRR 6.
LRR 6.
LRR 7.
LRR 7.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.5
Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
   AA;
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CXM3_CONPU
ID CXM3_CONPU
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P80251; P80257;
                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pp
  5;
                                                                                                                                                                                                                                                                                                                                                                                                                     Nielsen K.J., Watson M., Adams D.J., Hammarstroem A.K., Gage P.W.,
Hill J.M., Craik D.J., Thomas L., Adams D., Alewood P.F., Lewis R.J.;
"Solution structure of mu-conotoxin PIIIA, a preferential inhibitor of
persistent TTX-sensitive sodium channels.";
J. Biol. Chem. 277:0-0(2002).
-:- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
channel. This peptide causes flaccid paralysis in both mice and
fish. It blocks reversibly rat neuronal type II channel, whereas
it blocks irreversibly amphibian muscle Na+ channels (Probable).
-:- SUBCELULIAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxin; Neurotoxin; Sodium channel inhibitor; Hydroxylation; Amidation; Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- PTM: EXISTS in two forms, due to cis-trans isomerization at Hyp-8.
Adopts a predominately trans conformation (Probable).
-!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R->A: DECREASE IN AFFINITY TO CHANNEL F0E19F45BC97AC13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-26 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                         Safo P., Rosenbaum T., Shcherbatko A., Choi D.-Y., Han E., Toledo-Zral J.J., Olivera B.M., Brehm P., Mandel G.; "Distinction among neuronal subtypes of voltage-activated sodium channels by mu-conocxin PIIIR.";
                                                                                                                                                                                 Shon K.-J., Olivera B.M., Watkins M., Jacobsen R.B., Gray W.R., Floresca C.Z., Cruz L.J., Hillyard D.R., Brink A., Terlau H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                        "mu-Conotoxin PIIIA, a new peptide for discriminating among tetrodotoxin-sensitive Na channel subtypes.";
J. Neurosci. 18:4473-4481(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 27;
                                                                   Conus purpurascens (Purple cone).
Eukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYDROXYLATION (PROBABLE). HYDROXYLATION (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MU-CONOTOXIN PIIIA
                                                                                                                                        SEQUENCE FROM N.A., SYNTHESIS, AND MUTAGENESIS
             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mu-conotoxin PIIIA precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.9;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROBABLE)
                                                                                              Neogastropoda; Conoidea; Conidae; Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBABLE
                                                                                                                                                                                                                                                                              BINDING TO NEURONAL SODIUM CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CCN--GGCSSKXCRDHARCC 20
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                                                                                                                                                                                                                                                                                                                                                                  Neurosci. 20:76-80(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 CCGFPKSCRSRQCKPH-RCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 9; Conser
                                                                                                                                                       TISSUE=Venom duct;
PubMed=9614224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 AA;
                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR.
                                                                                                            NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12006587;
                                                                                                                                                                                                                                                                                              PubMed=10627583
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  P58925;
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71 AA.

PRT;

STANDARD;

MT21_MYTED

RESULT 8 MT21_MYTED

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-i- INDÚCTION: BY CADMIUM.
-i- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
PIT, S19420, S39420.
InterPro, IPR003019; Metallthion.
InterPro; IPR001008; Mtlthion_mlsc.
Pfam; PF00131; metalthio; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Digestive gland;
MEDLINE-99206055; PubMed=10190057;
Barsyte D., White K.N., Lovejoy D.A.;
"Cloning and characterization of metallothionein cDNAs in the mussel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94062828; PubMed=8243463; Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E., Kaeqi J.H.R., Fothergill J.E.; Kaeqi Guences of five dimeric and four monomeric forms of metallothionelin from the edible mussel Mytilus edulis."; Eur. J. Blochem. 218:183-194(1993).
                                                                                                                                                                                                                           Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E., Kaegi J.H.R., Pothergill J.E.;
"Complete amino acid sequences of five dimeric and four monomeric forms of metallothionein from the edible mussel Mytilus edulis.";
Eur. J. Biochem. 218:183-194(1993).
-!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR SEQUESTRATION OF TOXIC METAL IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                              Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mytilus edulis L. digestive gland.";
Comp. Blochen. Physiol. 122C:287-296(1999).
-!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
SEQUESTRATION OF TOXIC METAL IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metallothionein 20-1 isoforms A and B (MT-20-IA and MT-20-IB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 66 S -> A (IN MT-20-IB).
71 AA; 6944 MW; 4FD275FE34E81654 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metal-binding; Metal-thiolate cluster; Cadmium.
VARIANT 66 66 S -> A (IN MT-20-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 28, Created)
(Rel. 28, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NC-----CNGGCSSKXCR--DHARC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 NCIETNVCICGTGCSGKCCRCGDACKC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metallothionein 20-II (MT-20-II). Mytilus edulis (Blue mussel).
                                                                                                                                                                                                             MEDLINE=94062828; PubMed=8243463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00875; MTMOLLUSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 40.7 tes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               -! - SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel.
                                                                                                                                            NCBI_TaxID-6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994
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P80252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides 20:1139-1144(1999).
-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
SUBCELLUAR LOCATION: Secreted (By similarity).
SUBCELLUAR: Expressed by the venom duct.
SIRSUE SPECIFICITY: Expressed by the venom duct.
SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor; Signal; Amidation. 1 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                             6;
                                                                                                                                                                                                                                                                                                                                                     Score 48.5; DB 1; Length 71;
Pred. No. 3.9;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Vencom duct;

BEDLINE=20037955; PubMed=10573284;

Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;

"Conopeptides from Conus striatus and Conus textile by CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6493;
                                                                                                                                                                                                                                                                                                                    71 AA; 6887 MW; 4FD275FE39857654 CRC64;
                                                                                                                                                                                                                                                                             Metal-binding; Metal-thiolate cluster; Cadmium.
INIT_MET 0 0
SEQUENCE 71 AA; 6887 MW; 4FD275FE39857654 CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                           IPR001008; Mtllthion_mlsc.
                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NC-----CNGGCSSKXCR--DHARC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 NCIETNVCICGTGCSGKCCRCGDACKC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omega-type conotoxin SO3 precursor.
                                                                                                                                                                                     PIR; S39421; S39421.
InterPro; IPR003019; Metallthion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus striatus (Striated cone).
                                                                                                                                                                 EMBL; AJ005456; CAA06553.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF146348; AAD31908.1; -.
                                                                                                                                                                                                                                                                                                                                                         40.18;
40.78;
                                                                                                                                                                                                                       InterPro; IPR001008; Mtllth
Pfam; PF00131; metalthio; 1
PRINTS; PR00875; MTMOLLUSC.
                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 40.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CXO3_CONST
09XZK2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CXO3_CONST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roche P.J.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.
UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE CILLS, THEREBY REDUCING ITS RATE OF INFLUX FROM THE ENVIRONMENT INTO THE EXPRACELLULAR COMPARTMENT. STC ALSO STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 33-57.
MEDILNE-88083961; PubMed=3319739;
Butkus A., Roche P.J., Fernley R.T., Haralambidis J.,
Butkus A., Trandaris J.F., Traegar G.W., Coghlan J.P.;
Penschow J.D., Ryan G.B., Trahahir J.F., Treegar G.W., Coghlan J.P.;
Purification and cloning of a corpuscles of Stannius protein from
                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Stanniocalcin precursor (STC) (Corpuscles of stannius protein) (CS)
                                                                 AMIDATION (G-71 PROVIDE AMIDE GROUP)
                                                                                                                                                                  .;
0
                                                                                                                                DB 1; Length 71; 4.5;
                                                                                                                                                                  5; Indels
 OMEGA-TYPE CONOTOXIN SO3.
                                                                                  (POTENTIAL).
CE7070DCE3094D73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: CORPUSCLES OF STANNIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
STANNIOCALCIN.
BY SIMILARITY.
                 BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                  0; Mismatches
                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISPOSAL INTO BONE AND SCALES. SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anguilla australis.";
Mol. Cell. Endocrinol. 54:123-133(1987).
                                                                                                                                Score 48;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anguilla australis (Australian eel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR000978; Stanniocalcin.
Pfam; PF03298; Stanniocalcin; 1.
Hormone; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M36967; AAB91483.1; -.
                                                                                                                                  39.7%;
58.3%;
                                                                                                 7628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    (Hypocalcin) (Teleocalcin).
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
250
58
 70
61
65
70
70
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                                                                                                                                                                                                   2 NCCNGGCSSKXC 13
                                                                                                                                                                                                                                   59 NCCTGSCRSGKC 70
                                                                                                               Query Match
Best Local Similarity
7; Conserve
                                                                                                 71 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7940;
                                                                                                                                                                                                                                                                                                                  STC_ANGAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS.
PEPTIDE
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
DISULFID
                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anguilla.
                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                     STC_ANGAU
 FT
FT
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SO
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                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Post-translationally modifies flagellin by methylation of epsilon amino group of surface-exposed lysine residues (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ho K.C., Chang G.N.; "The fliu and fliv genes are expressed as a single ORF in Salmonella
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (PROBABLE).
W, BB972BD951F75B3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella cholerae-suis (Salmonella enterica).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lysine-N-methylase (EC 2.1.1..) (Lysine N-methyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLIB_SALTY STANDARD; PRT; 401 AA. 056106; Q56087; 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation Property Prince N-methylase (EC 2.1.1.-) (Lysine N-methylase) FLIB OR NML OR STM1958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.7%; Score 48; DB 1; Length 401;
                                                                                                                           Score 48; DB 1; Length 250;
                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C42D82DF67EDBD10 CRC64;
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                                                                                                                                       Pred. No. 12;
}; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE FLIB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Can. J. Microbiol. 46:1149-1152(2000)
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CH12440 / Serotype C1;
MEDLINE=21022014; PubMed=11142406;
                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Methyltransferase.
SEQUENCE 401 AA; 45366 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF159460; AAF80753.1; -.
                                                                           61 I
27174 MW;
                                                                                                                                                                                 3 CCNG----GCSSKXCRDHARC 19
                                                                                                                                                                                                                 44 CLNGALQVGCSAFACLDNSTC 64
                                                                                                                       39.78;
                                                                                                                                       42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%;
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 CSGSACRDH--CC 27
53
64
97
134
201
201
61
250 AA;
                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        choleraesuis.
                                                                                                                                                                                                                                                                                                                                                                                     FLIB OR FLIU
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Q9KJV4;
              DISULFID
DISULFID
 DISULFID
                                            DISULFID
                                                           DISULFID
                                                                                       SEQUENCE
                                                                           CARBOHYD
                                                                                                                       Query Match
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FLIB_SALTY
                                                                                                                                                                                                                                                                            FLIB_SALCH
                                                                                                                                                      Matches
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FT
FT
FT
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SO
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nauyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Waterston R., Wilson R.K., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                 "The flagellin N-methylase gene fliB and an adjacent serovar-specific IS200 element in Salmonella typhimurium."; Microbiology 143:1539-1547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
--- FUNCTION: Post-translationally modifies flagellin by methylation of epsilon amino group of surface-exposed lysine residues.
--- SIMILARITY: BELONGS TO THE FLIB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99228399; PubMed=10213385;
Barlow A.J., Bogardi J.P., Ladher R., Francis-West P.H.;
"Expression of chick Barx-1 and its differential regulation by FGF-8
and BMP signaling in the maxillary primordia.";
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                       SEQUENCE FROM N.A.
STRAIN=LTZ / ATCC 23564, and 168-94;
MEDLINE=97311993; Pubmed=9168604;
Burnens A.P., Stanley J., Sack R., Hunziker P., Brodard I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.7%; Score 48; DB 1; Length 401; 61.5%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Methyltransferase; Complete proteome.
SEQUENCE 401 AA; 45414 MW; C3CAB7A8E3C9F563 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homeobox protein BarH-like 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, 254217; CAA90951.1; -.
EMBL, 267149; CAA31562.1; -.
EMBL, AE000787; AAL20870.1; -.
$tyGene, SG10575; fliB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27
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nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 CSGSACRDH--CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                     NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRX1_CHICK
Q9W6D8;
                                                                                                                                                                   Nicolet J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRX1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BARX1
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 Q
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                             CRANICRACIAL DEVELOPMENT, IN ODOMYOGENESIS AND IN STONACH ORGANOGENESIS. MAY HAVE A ROLE IN THE DIFFERENTIATION OF MOLARS ORGANOGENESIS. MAY HAVE A ROLE IN THE DIFFERENTIATION OF MOLARS SUBCELLUIAR LOCATION: Nuclear (Probable).

TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE FACIAL FRIMORDIA, DEVELOPMENTAL STAGE: FIRST DETECTABLE IN THE FACIAL STAGE: FIRST DETECTABLE IN THE FACIAL PRIMORDIA AT STAGE: FIRST DETECTABLE IN THE FACIAL PRIMORDIA AT STAGE IN AFTER NUCLEAR MID-AND HINDRALIN. EXPRESSED IN REGIONS DERIVED FROM BOTH MID-AND HINDRALIN BURNAL CREST. ALSO EXPRESSED IN THE DEVELOPING CARTILAGE ELMENTS OF THE LIMB, FIRST WITHIN A RESTRICTED POPULATION IN THE PRECHONDROGENIC MESENCHYME AND LATER IN THE ROUNDED CHONDROCYTES AT THE EPIPHYSES OF DEVELOPING LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%; Score 47.5; DB 1; Length 207; 60.0%; Pred. No. 12;
Dev. Dyn. 214:291-302(1999).
-!- FUNCTION: TRANSCRIPTION FACTOR, WHICH MAY BE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3EDE64A91D3BCE84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homeobox; Transcription; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Channel catfish virus: a new type of herpesvirus."; virology 186:9-14(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Ictalurid Herpes-like viruses.
                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE BAR HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical gene 13 zinc-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRANSFAC; T03934; -.
InterPro; IPR000047; HTH_repressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92087490; PubMed=1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0024; HOMEOBOX.
PRINTS; PRO0031; HTHREPRESSR.
PRODOM; PD0000010; HOMEOBOX; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 AA; 22467 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF116460; AAD21043.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 39.3
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 GGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GSCSSSGCR---RCC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T03934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Auburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davison A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VG13_HSVI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
VG13_HSVI1
 δλ
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7
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                   38.8%; Score 47; DB 1; Length 82; 38.5%; Pred. No. 6.7;
                                                                                                                                                     EMEN: W75136; AAA88116.1; -.
PIR; E36787; E36787.
Hypothetical protein; Zinc; Zinc-finger.

Hypothetical protein; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                      Pred. No. 6.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        completed: January 10, 2003, 08:32:58
                                                                                                                                                                                                                                                                                                                               2 NCCN-----GGCSSKXCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                        10 NCCNPMSLLCGGGCDLISC----CC 30
                                                                                                                                          EMBL; M75136; AAA88194.1; -.
                                                                                                                                                                                                                                                                        38.5%;
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          : 4.30435 secs
                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                              Matches
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Job time
           δλ
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January 10, 2003, 08:32:32 ; Search time 12 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                        OM protein - protein search, using sw model
                                                                                                                                       Run on:
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(without alignments)
343.412 Million cell updates/sec US-09-910-009A-211 121 1 XNCCNGGCSSKXCRDHARCC 20 Perfect score: Sequence:

Scoring table:

671580 seqs, 206047115 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* Sp_archea:*
Sp_bacteria:*
Sp_fungi:*
Sp_lungi:*
Sp_human:*
Sp_manmal:*
Sp_mcanelle:*
Sp_phage:*
Sp_phage:*
Sp_phage:*
Sp_phage:*
Sp_phage:*
Sp_phage:*
Sp_phage:* SPTREMBL_21:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	09feff oryza sativ 09vr08 drosophila 09vr08 drosophila 06220 mus musculu 064507 mus musculu 09elt7 avian infec 01456 homo sapien 096874 entamoeba h 08wsw3 tetrahymena 004500 arabidopsis 084x9 oryza sativ 09u147 leishmania 070619 sus scrofa 08qgn9 brachydanio 08qgn9 brachydanio 08qgn9 brachydanio 08qgn9 brachydanio 08qgn9 brachydanio
ID	Q9FEF3 Q9VR08 Q6Z220 Q64507 Q9ELT7 Q14564 Q9WSW3 Q90450 Q9U147 Q9U147 Q9U147 Q9CGN9 Q9V7V5
DB	10 2 2 1 11 11 11 10 10 10 13 3 3
% Query Match Length DB	550 3680 48 223 233 230 169 169 1122 389 801 621 1245
% Query Match	46.7 444.6 444.2 443.8 443.0 443.0 443.0 441.3 441.3 440.9 40.9
Score	56.8 8.55.8 8.55.8 8.50.8 8 8.50.8 8.50.8 8 8.50.8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
Result No.	13 9 9 10 10 11 11 12 11 14 11 16

QQ οy

Q8xr01 ralstonia s Q9vul2 drosophila Q90wml rana catesb Q9st61 solanum tub Q8s289 orvas sariv	Q9xvx3 cenorhabdi Q22048 ceenorhabdi Q95qy1 ceenorhabdi Q95qy8 homo sapien Q17641 ceenorhabdi	Q9byrO homo sapien O22499 zea mays (m Q9n6n6 conus stria Q9ncv4 conus stria		Q18238 caenorhabdi Q70148 rattus norv Q90wm0 bufo japoni Q9jix1 rattus norv Q41064 pisum sativ Q9ave7 oryza sativ Q2652 strongyloce Q8wx98 homo sapien 008999 mus musculu
Q8XR01 Q9VU12 Q90WM1 Q9ST61 Q8S289	Q9XVX3 Q22048 Q95QY1 Q9BYQ8 Q17641	Q9BYR0 O22499 Q9N6N6 Q9NCV4	09NCV3 09NCV2 09NCV1 09NCV0 P91526	Q184.58 Q70148 Q90WM0 Q9JJX1 Q41064 Q9AVE7 Q26632 Q8WX98
13 03 10 00	00000	40000	000000000000000000000000000000000000000	
	24917	4 (14 / 4 / 4 / 4	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	044444
18 27 35 46	152 164 166 191 197	124 60	66 66 66 1372	188 353 379 464 626 1297 1311 1833
40.5 40.5 40.5 40.5	40.1 40.1 40.1 40.1	40.1 39.7 39.7	399.7 399.7 7.998 7.998 7.998	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
4 4 4 4 4 0 0 0 0 0		4 4 8 6 7 . 8 8 4 8 8 8 9		
17 18 19 . 20 21	22 23 25 26	22 28 30 30 31		38. 39. 44. 54. 54.

ALIGNMENTS

RES Q9F ID AC	RESULT 1 Q9FEF3 ID Q9FEF3;	PRELIMINARY;	•~	PRT;	550 AA.					
272	01-MAR-2001 01-MAR-2001	(TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16,	16, 1	Created) Last sequence update) Last annotation update)	ence up	date) update	<u>.</u>			
G C	P0888A04.4 protein (P0006C01.19 protein). P0688A04.4 OR P0006C01.19.	rotein (P00 R P0006C01.	06C01 19.	.19 prote	in).					
8 0 0	Oryza sativa (Rice). Eukaryota: Viridiplantae: Streptophyta: Emhrvochyta: Trachsochuta:	(Rice).	e; St.	reptophyt	a: Embr	tydnov.	. e.	, daood	a	
88	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza,	a; Magnolio e; Oryzeae;	phyta Oryza	Lilliops	ida; Pc	ales;	Poaceae	;;	,	
N S	NCBI_TaxID=4530;	530;	•							
RP	SEQUENCE FROM N.A.	M N.A.								
RC	STRAIN-CV. NIPPONBARE;	IPPONBARE;								
RA	Sasaki T., Matsumoto T., Yamamoto K.;	atsumoto T.	, Yama	amoto K.;						
RT	"Oryza sativa n	Sativa nipponbare(GA3) genomic DNA, chromosome 1,	e(GA3)	genomic	DNA, C	hromos	ome 1,	PAC		
RL	Submitted (AUG-2000) to the FMRI/GenBank/DDDT databases	UG-2000) to	+ h	WRI./GenB	מתת/ לוחה	+ + 1	000			
RN	[2])	7	ממט (אווש	ממרמ	Dasas.			
RP	SEQUENCE FROM N.A.	M N.A.								
RC	STRAIN-CV. NIPPONBARE;	IPPONBARE;								
RA	Sasaki T., Matsumoto T., Yamamoto K.;	atsumoto T.	, Yama	umoto K.;						
RT	"Oryza sativa n	Sativa nipponbare(GA3) genomic DNA, chromosome 1,	e(GA3)	genomic	DNA, C	hromos		PAC		
F.	Submitted (JUL-2000) to the FMRI./GenBank/DDB1 databases	UL-20001 to	t he	MRI./GenB	ant/ /nn	ال 1000 -	o o o e d			
DR	EMBL; AP0028	39; BAB1909	3.1;	יייניביו ספיווד	מטט (אוווי	o da ca	Dases.			
DR	002	44; BAB1907	7.1;							
Š Š	SEQUENCE 5:	550 AA; 6020	60263 MW;		1DE6F1BBA8B9E8A1 CRC64;	8A1 CR	C64;			
ÒM	Query Match Best Local Similarity		46.78;	Score 56.5; DB 10;	.5; DB		Length 550;	550;		
Σ	Matches 9; (vat	ì	2; Mismatches	tches	5;	Indels	1;	Gaps	

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SEQUENCE FROM N.A
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DR
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SO
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RA Admantalege FOG., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Admantides G.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Admantides G.G., Scherer S.E., Holt R.A., Edwiss R.A., Galle R.F.,

RA George R.A., Lewis S.E., Holt R.A., Albhurner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,

RA Ballew R.M., Benos P.V., Bernan B.P., Bhandarl D., Bollaharo S.,

RA Berson K.Y. Benos P.V., Bernan B.P., Bhandarl D., Bolshakov S.,

RA Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottler P.,

RA Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottler P.,

RA Borkova D., Botchen M.B., Buller H., Cadieu B., Center A., Chandra I.,

RA Borkova D., Botchen A., Deng Z., Mays A.D., Dew I., Dischakov S.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dorlo L.E., Downes M., Dayan R.A., Chandra I.,

RA Borkova D., Botchen A., Gony F., Gorrell J. H., Gablat W., Capter S.,

RA Glodek A., Gony F., Gorrell J. H., Gu Z., Galbat I.M., Ralush R.,

RA Harris N.L., Harvey D., Heiman T.J., Herrandez J. R., Houck J.,

RA Jalai M., Kalush F., Katpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Murphy B., Murphy L., Mazny D.M., Nelson D.K.,

RA Alazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Paches M.,

RA Shien E., Spradling A.C., Stapleton M., Strong K., Sun E.,

RA Spiert K., Penington K., Saudlers R., Well W., Smith H.O.,

RA Wang Z.-Y., Wassarman D.A., Wellscock G.M., Well W., Smith H.O.,

RA Wang Z.-Y., Wassarman D.A., Well W., Zhon G., Zhu X., Smith H. Sheng S. Libeng X.H., Robogsof W., Raping G., Yon C., Stapleton M., Shon G., Sheng L., Sheng K
                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                           01-MAX-2000 (TrEMBLrel. 13, Created)
01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                PRT; 3680 AA
                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003576; AAF51000.1; -. HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD003573, ET; 1.
SMART; SM00179; EGF_CA; 16.
SMART; SM00201; EGF_11ke; 35.
SMART; SM00274; FOLN; 5.
SMART; SM00289; WRI; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002603; ET.
InterPro; IPR003645; FolN.
InterPro; IPR002899; WRI/EB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0000488; dp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00008; EGF; 25.
                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                             CG15637 protein.
DP OR CG15637.
                                                                                                                                                                                                                                    NCBI_TaxID=7227;
                                                                              Q9VR08;
                                                                   Q9VR08
                                   RESULT 2
Q9VR08
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1;
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                       PROSITE; PSO0022; EGF_1; 1.
PROSITE; PS01186; EGF_2: 18.
PROSITE; PS01187; EGF_CA: 17.
Calcium-binding; EGF-Like domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 3680 AA; 388637 MW; E5E972E1A3479EFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
"Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans.";
Interesting of Mycoplasma fermentans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma fermentans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.2%; Score 53.5; DB 2; Length 48; 42.1%; Pred. No. 0.21; tive 3; Mismatches 7; Indels
                                                                                                                                                           44.6%; Score 54; DB 5; Length 3680; 57.1%; Pred. No. 7.2; 2; Indels iive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F15567.1; -. 5319 MW; 668836FA3592B2C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Serine 2 ultra high sulfur protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence during insertion.",
J. Bacteriol. 181:7597-7607(1999).
EMBL; AF179376; AAF15567.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20069643; PubMed=10601219;
PROSITE; PS00010; ASX_HYDROXYL; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99115554; PubMed=9916088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 SCCSSCCKEK-CRKECKCC 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                   3294 GGCSSKPCGENSKC 3307
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                                                                                                                                                                                                                                                                       6 GGCSSKXCRDHARC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=PG18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9RFP5;
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TISSUE-TESTIS;
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SEQUENCE
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                                           Q9ELT7
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Q14564
                     RESULT 6
                                29ELT7
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                                                                                                                Wood L., Mills M., Hatzenbuhler N., Vogeli G.;
"Additions and Corrections: Serine-rich ultra high sulfur protein gene expression in murine hair and skin during the hair cycle.";
J. Biol. Chem. 266:4024-4024(1991).
EMBL; M37760; AAA40107.1;
HSSP; P01064; 1P12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/C;
MEDLINE=91065960; PubMed=2250030;
Wood L., Mills M., Hatzenbuhler N., Vogeli G.;
"Serine-rich ultra high sulfur protein gene expression in murine hair and skin during the hair cycle.";
J. Biol. Chem. 265:21375-21380(1990).
STRAIN=BALB/C;
MEDIINE-91065960; PubMed=2250030;
Wood L., Mills M., Hatzenbuhler N., Vogeli G.;
"Serine-rich ultra high sulfur protein gene expression in murine hair and skin during the hair cycle.";
J. Biol. Chem. 265:21375-21380(1990).
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                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 0.96;
                                                                                                                                                                                                                                                                    43.8%; Score 53; DB 11; Length 223; 44.4%; Pred. No. 0.94;
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                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                            HSSP; P01064; 1F12.
MGD; MGT:1354758; Krtap5-4.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001007; VWF_C.
PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_2.
PROSITE; PS01208; VWFC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21781 MW; 6CC50B41B2137C23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Serine 1 ultra high sulfur protein.
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PROSITE; PSO1177; ANAPHYLATOXIN 1: UNKNOWN_1.
PROSITE; PSO1277; ANAPHYLATOXIN 1: UNKNOWN_1.
PROSITE; PSO1208; UNFC; UNKNOWN 3.
SEQUENCE 230 AA, 21781 MW; 6CC50B41B2137C23
                                                                                                                                                                                                                                                                                                                                                                                                        230 AA
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                                                                                                                                                                                                                                                                                              3; Mismatches
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HSSP; P01064; 1PP2.
INCEPPO: JPR001450; AF48_ferredoxin.
InterPro: JPR001450; AF48_ferredoxin.
InterPro: JPR001305; DnaJ_CXXCXGXG.
InterPro: JPR001305; DnaJ_CXXCXGXG.
InterPro: JPR001007; VWP_C.
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                                                                                                       MEDLINE=91154184; PubMed=1840598;
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                                                                                                                                                                                                                                                                                                                                  159 CCSSGCGSSCCO--SSCC 174
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Best Local Similarity
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                                                                                 SEQUENCE FROM N.A.
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                                                                                              STRAIN=BALB/C;
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                                                                                                                                                                                                                                                                                                                                                             Callison S.A., Jackwood M.W., Hilt D.A.; Callison S.A., Jackwood M.W., Hilt D.A.; Genotypic characterization of foreign infectious bronchitis virus isolates and comparison with U.S. isolates."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. BMBL; AFSB467, AAG01338.1; I.InterPro: IPR02551; Corona_S1: 1.
                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
NCBI_TaxID=11120;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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"Nucleotide sequence of a Human high-sulphur keratin cDNA.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
BEMBL: X63755; CAA45283.1;
HSSP; P01064; 1P12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.8%; Score 53; DB 12; Length 539;
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InterPro; IPR001007; WPF_C.
PROSITE: PS01186: ESF_2; UNKNOWN_1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS01208; WPFC; UNKNOWN_2.
PROSITE; PS01208; WPFC; UNKNOWN_2.
SEQUENCE 169 AA: 16216 MW; A39206EB0B49D4BE CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                             Surface glycoprotein S1 (Fragment).
PRT;
                                                                                                                                                                                 Avian infectious bronchitis virus.
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InterPro; IPR001138; Fungi_TrN.
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 NGGCKQSVWQGHATCC 372
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PRELIMINARY;
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Homo sapiens (Human).
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Matches 8; Conserv
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PRT;
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                              01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 40.9
Matches 9; Conservative
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NCCNGGCSSKXCRDHA 17
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                                                                       F21M12.17 protein.
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                                                                                                                                                         NCBI_TaxID=3702;
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SEQUENCE
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY061892; AAL31645.1;
SEQUENCE 162 AA: 16757 MW; 9B2DB3C95981FFCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
NCBI_TaxID=5911;
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                                                                                                                                                                                                                                                                                                                                                                                                          43.0%; Score 52; DB 5; Length 231; 38.9%; Pred. No. 1.4;
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                                                                                                                                                                                                                                      STRAIN=HM1:IMSS;
Rosales-Encina J.L., Jimenez-Delgadillo B.;
"Entamoeba histolytica 30 kDa collagen binding protein.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U67157; AAD09522.1; -.
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SEQUENCE 231 AA; 26066 MW; 1385DBD6219CC168 CRC64;
                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                        30 kDa type I collagen binding protein (Fragment).
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                                                                                                            (TrEMBLrel. 10, (TrEMBLrel. 17,
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87 CCSSGCGSSCCQ--CSCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CCNGGCSSKXCRDHARCC 20
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Best Local Similarity 38.9*
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                                                                    PRELIMINARY;
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Entamoeba histolytica
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ses 10; Conserva
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01-JUN-2001
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Vysotskala V.S., Osborne B.I., Toriumi M., Yu G., Oji O., Shen Y.K.,
Araujo R., Au M., Buehler E., Conway A.B., Conway A.R., Dewar K.,
Feng J., Kind C., Kurtz D., Li Y., Shinn P., Sun H., Davis R.W.,
Ecker J.R., Federspiel N.A., Theologis A.
"The sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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"Molecular cloning of salt responsive gene in rice, OSSRIII.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF366556; AAM00365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.1%; Score 51; DB 10; Length 454; 50.0%; Pred. No. 3.5; cive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.3%; Score 50; DB 10; Length 122; 40.9%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. COLUMBIA;
Theologis A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC000132; AAB60732.1; -.
SEQUENCE 454 AA; 51434 MW; 0A3F8FD93EA2AD4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 122
122 AA; 12548 MW; CE1069483109BF18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01.JUN-2002 (TrEMBLrel. 21, Created)
01.JUN-2002 (TrEMBLrel. 21, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
Saline responsive OSSRIII protein (Fragment).
                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 AA.
   454 AA
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                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
                                                                Created)
PRT;
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OBOGN9;
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Q9Y7V5
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        DOR KWW KWW SQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                            Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).
EMBL; AL121861; CAB58387.1; -.
HSSP; P38197; 1B54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 5; Length 389;
Pred. No. 4.4;
1; Mismatches 5; Indels
                                                                                                                                                                                                                          STRAIN=FRIEDLIN;
Aber E., Volckaert G., Ivens A.C., Lawson D., Quail M.,
Rajandream M.A., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42606 MW; 9FA2E61700590569 CRC64;
               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Possible proline synthetase associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Low density lipoprotein receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                801 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR0010033; Ldl_receptor_rep.
InterPro; IPR002172; LDL_recept_A.
Pfam; PF00008; EGF; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFGM: PF01168; UPF0001; 1.
TIGRRAMS; TIGRO0044; UPF0001; 1.
PROSITE; PS00118; PAZ_HIS; UNKNOWN_1.
PROSITE; PS01211; UPF0001; 1.
SEQUENCE 389 AA; 42606 MW; 9FAZE6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001211; PhospholipaseA2.
InterPro; IPR001608; UPF0001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=FRIEDLIN;
MEDLINE=98146435; PubMed=9477341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=LIVER;
MEDLINE=98215582; PubMed=9556295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4%
Best Local Similarity 44.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                        Leishmania major.
                                                                                                                                                               NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
                                                                                                                                            Eukaryota;
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ACCOORDINATIONS OF THE PROPERTY OF THE PROPERT
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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cadieux B., Joly L., James S., Ekker M., Bennett H.P.J.;
"Identification of Members of the Zebrafish Granulin Gene Family:
"stience for Two Classes Displaying Different Architectures.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR375477; AAM00265.1;
NON_TER 621 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                      SNART; SM00129; EGE_11ke; 2.
SNART; SM00199; EGE_11ke; 2.
SNART; SM00191; EGE_11ke; 2.
SNART; SM00192; LDLa; 7.
SNART; SM001195; LDLa; 7.
PROSITE; PS00101; ASX_HYDROXXL; 2.
PROSITE; PS01186; EGE_CA; 1.
PROSITE; PS01187; EGE_CA; 1.
PROSITE; PS0109; LDLRA_1; 7.
Calcium-binding; EGE_CA; 1.
Calcium-binding; EGE_11ke domain; Glycoprotein; Hydroxylation; Lipoprotein; Receptor; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trichoderma harzianum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales: mitosporic Hypocreales; Trichoderma.
NCBI_TaxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               801 AA; 88722 MW; 4D58D60CF25736A3 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
conidiospore surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.9%; Score 49.5; DB 13;
40.9%; Pred. No. 7.8;
iive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.3%; Score 50; DB 6; Best Local Similarity 43.5%; Pred. No. 8.1; Matches 10; Conservative 1; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -;
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Pfam; PF00057; ldl_recept_a; 7. Pfam; PF00058; ldl_recept_b; 5. PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 DCENGSDEEGCSPKTCSQDEFCC 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 9; Conservative
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NCBI_TaxID=7955;
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NON_TER
SEQUENCE
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RP SECUENCE FROM N.A.

RC STRAIN-ATCC 32173;

RA MEDIATE-9343481: PubMed=10413618;
RA Van Montagu M., Benhamou N., Ponce Noyola P., Bauw G., Ziv T.,
RA Van Montagu M., Herrera Estrella A., Horwitz B.A.;
RT Povelopmental regulation of cmpl, a gene encoding a multidomain
RT Conidiospore surface protein of Trichoderma.";
RL Fungal Genet. Biol. 27:88-99(1999).
DR EMBL; AJ133651; CAB40845.1; -.
DR EMBL; AJ133651; CAB40845.1; -.
DR HSSP; POII80; INPO.
DR InterPro; IPR001673; S_mold_repeat.
DR PROSITE; PS01346; CLAUDIN; UNKNOWN_1.
SQ SEQUENCE 1245 AA; 135824 MW; 3349C749AFAOCDF8 CRC64;
Query Match
Query Match
A0.9%; Score 49.5; DB 3; Length 1245;
Best Local Similarity 45.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 5; Indels 3; Gaps
Qy 3 CCNGGCSSK---XCRDHARC 19
| | | | | | | | | | | | | | | | | |
Db 497 CFDGSCKSKENNKCRDNRQC 516
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Search completed: January 10, 2003, 08:37:37 Job time : 14 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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January 10, 2003, 08:32:27; Search time 3.30435 Seconds (without alignments) 251.041 Million cell updates/sec Run on:

US-09-910-009A-432 134 1 ZNCCNGGCSSKWCRDHARCC 20 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	;	QI	KRUB_HUMAN	KRUA_HUMAN	MT1_CANGA	GRN_CAVPO	ORYB_ORYSA	GPCR_LYMST	MT1A_HORSE	MT21_MYTED	MT22_MYTED	CXO5_CONTE	HGDA_ACIFE	OXLA_NEUCR	CXM3_CONPU	AHM2_ARATH	ALK1_PIG	BIR1_HUMAN	BRX1_CHICK	GRN_HUMAN	MT2_CAEEL	CXO3_CONST	MSMB_STRCA	WFD2_HUMAN	CYSL_LYCES	CMGA_BACSU	TPA_BOVIN	CTA4_HUMAN	LMG3_MOUSE	LMG3_HUMAN	MT14_MYTED	MT1A_MYTED	MT1B_MYTED	TRGS_TACTR	
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1;

Gaps

2;

Query Match
39.6%; Score 53; DB 1; Length 194;
Best Local Similarity 44.4%; Pred. No. 3.9;
Matches 8; Conservative 3; Mismatches 5; Indels

3 CCNGGCSSKWCRDHARCC 20 | | | | | | | : | | | 16 CCSSGCGSSCCQ--SSCC 175

Οy

RESULT 2 KRUA_HUMAN

061483 mus musculu P18301 angulla au P54190 toxocara ca 09kjv4 salmonella 056106 salmonella 0600548 homo sapien 09bkq8 caenorhabdi P7853 homo sapien 0920f8 mus musculu 0921k9 rattus norv
1 DLL1_MOUSE 1 STC_ANGAU 1 FL26_TOXCA 1 FL1B_SALCH 1 MCRA_METJA 1 MCRA_METJA 1 DD13_CAEEL 1 AD17_HWAN 1 AD17_RAT
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ALIGNMENTS

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us-09-910-009a-432.rsp

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Metallothionein-I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRN_CAVPO
P28797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INIT_MET
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
GRN_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           keratin genes.";
Gene 227:137-148(1999).
1- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDEEMAL DERIVATIVES
SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
SULFUR AND HIGH-TROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
6-20 kDa, WHERBAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
KERATINS (40-56 kDa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION.
-i- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perez C., Auriol J., Gerst C., Bernard B.A., Egly J.-M.; "Genomic organization and promoter characterization of two human UHS
                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, ultra high-sulfur matrix protein A (UHS keratin A) (UHS
                                                                                                                                                                                                                                                                                                                                                            MCKinnon P.J., Powell B.C., Rogers G.E.; "Structure and expression of genes for a class of cysteine-rich proteins of the cuticle layers of differentiating wool and hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.8%; Score 52; DB 1; Length 169; 44.4%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keratin, Repeat, Multigene family.
SEQUENCE 169 AA; 16276 MW; 219B14FEEB49D4AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RICH (SR) REPEATS.
-!- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .ANGA
MTI_CANGA Siring
PISI13;
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
         169 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99148005; PubMed=10023043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell Biol. 111:2587-2600(1990).
                                                                                                                                                                                                                                                                                                                                              MEDLINE=91115951; PubMed=1703541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ006693; CAA07189.1; -. HSSP; P01064; 1PI2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X55293; CAA39005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 CCSSGCGSSCCQ--CSCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CCNGGCSSKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:6409; KRN1.
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                              TISSUE-Follicle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 148021; -.
                                                                                                                                                                  KRN1 OR UHSK1.
             KRUA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                           follicles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
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             $$ \text{$\frac{1}{2}$ \\ \frac{1}{2}$ \\ \fra
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                                                                                                                                                                                                    MEDLINE-90062075; PubMed=2584191; Mehra R.K., Garey J.R., Butt T.R., Gray W.R., Winge D.R.; Candida glabrata metallothioneins. Cloning and sequence of the genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITNE-89957829; PubMed-3194392;
Mehra R.K., Tarbet B.E., Gray W.R., Winge D.R.;
Mehra-specific synthesis of two metallothioneins and gamma-glutamyl peptides in Candida glabrata.";
Perc. Natl. Acad. Sci. US.A. 85:8815-8819(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogranio) [Contains: Granulin 1; Granulin 2;
Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavia porcellus (Guinea pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUESTRATION OF TOXIC METAL IONS.
-!- INDUCTION: BOTH MT-I AND MT-II GENES ARE REGULATED BY COPPER IN A CONCENTRATION-DEPENDENT FASHION, AND BOTH ARE INDUCIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILVER BUT NOT BY CADMIUM SALTS.
-!- MISCELLANEOUS: MT-I MIGHT BIND APPROXIMATELY 11-12 MOL EQ OF
candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51.5; DB 1; Length 62; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metal-binding; Metal-thiolate cluster; Copper; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80D768C06C44F7A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 4-21.
TISSUE-Testis;
                                                                                                                                                                                                                                                                                                          and characterization of proteins.";
J. Biol. Chem. 264:19747-19753(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J05133; AAA35272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 AA; 6243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A31252; A31252.
PIR; A34484; A34484.
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Matches 9; Conserv
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                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-16.
MEDLINE=89057829;
                                                                                                             NCBI_TaxID=5478;
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                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe H., Abe K., Emori Y., Hosoyama H., Arai S.;
"Molecular cloning and gibberellin-induced expression of multiple cysteine proteinses of rice seeds (oryzains).";
cysteine proteinses of rice seeds (oryzains).";
J Biol. Chem. 266:16897-16902(1991).
-: TISSUE SPECIFICITY: EXPRESSED ONLY IN SEEDS.
-: INDUCTION: BY GIBBERELLIC ACID (GA).
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRANULIN 7.
N-LINKED (GLCNAC. .) (POTENTIAL).
EE7C9FC8F21CB8A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 11;
              Baba T., Hoff H.B. III, Nemoto H., Lee H., Orth J., Arai Y., Gerton G.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last Sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Oryzain beta chain precursor (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              GRANULIN 1.
GRANULIN 2.
GRANULIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                      GRANULIN 4.
GRANULIN 5.
GRANULIN 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50.5;
                                                                                                                                                                                                                                                                                                                                                                                    ACROGRANIN.
                                                                                                                                                                                                                                                                                                                                          Cytokine; Repeat; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 QTCCRLQ-SGKWGCCPFPKAVCCEDHVHCC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Nipponbare; TISSUE=Seed;
MEDLINE=91358494; PubMed=1885617;
MEDLINE=93228994; PubMed=8471244;
                                                                                                                                                                                                                                                                                  InterPro; IPR000118; Granulin. Pfam; PF00396; granulin; 7. SMARF; SM00277; GRAN; 6. PROSITE; PS00799; GRANULINS; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62586 MW;
                                                                                                                                                                                                                                                                     EMBL; M86735; AAA37030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             ?164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   7376
439
7518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4530;
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P25777;
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CARBOHYD
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PEPTIDE
PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
67-protein coupled receptor GRLI01 precursor.
Lymnaea stagnalis (Great pond snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN A SMALL NUMBER OF
NEURONS WITHIN THE CENTRAL NERVOUS SYSTEM AND TO A LESSER EXTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tensen C.P., van Kesteren E.R., Planta R.J., Cox K.J.A., Burke J.F., van Heerikhuizen H., Vreugdenhil E.; "A G protein-coupled receptor with low density lipoprotein-binding motifs suggests a role for lipoproteins in G-linked signal
                                                                                                                                                                                                                                                                                                                                                                                                                            ORYZAIN BETA CHAIN.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4:
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Proc. Natl. Acad. Sci. U.S.A. 91:4816-4820(1994).
-!- FUNCTION: MIGHT DIRECTLY TRANSDUCE SIGNALS CARRIED BY LARGE EXTRACELLULAR (LIPO)PROTEIN(COMPLEXE)S INTO NEURONAL EVENTS.
                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 471;
                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Thiol protease; Symogen; Glycoprotein; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBF39D33995CEB1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                           PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                             InterPro; IPR000169; SHprot_acsite
                                                                                                                                                                                                                                           Pfam: PF00112; Peptidase_C1; 1.
Pfam: PF00396; granulin; 1.
PrNURS; PR00705; PAPAIN.
Probom: PD000158; Peptidase_C1; 1.
SMART; SM00277; GRAN; 1.
                                                                                                                                                                                               InterPro; IPR000118; Granulin.
InterPro; IPR000668; Peptidase_C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94255418; PubMed=8197140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50505 MW;
                                                                                                                               EMBL; D90407; BAA14403.1; -. PIR; JU0389; KHRZOB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.3%;
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164
301
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NCBI_TaxID=6523;
                                                                                                                                                              HSSP; P00785; 2ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 AA;
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                                                                                                                                                                                 MEROPS; C01.029;
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P46023;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 X 40 AA APPROXIMATE TANDEM REPEATS
SIMILAR TO THE LDL-RECEPTOR CLASS A.
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 9.
LDL-RECEPTOR CLASS A 9.
LDL-RECEPTOR CLASS A 10.
LDL-RECEPTOR CLASS A 11.
LDL-RECEPTOR CLASS A 12.
LRR 1.
                                                                                                                                                                                       DR PIR; $40241; $40241.

DR HSSP; $07954; 1CR6.

DR HSSP; $07954; 1CR6.

DR HSSP; $07954; 1CR6.

DR InterPro; IPR001275; DLL_recept_A.

DR InterPro; IPR001272; LDL_recept_A.

DR InterPro; IPR001372; LLR_ver.

DR InterPro; IPR001392; LRR_ver.

DR InterPro; IPR001392; LRR_ver.

DR Pfam; PF00107; LAL_i: 1.

DR Pfam; PF00107; LAL_i: 1.

DR Pfam; PF00107; LRR; 6.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR SMART; SM00192; LDLR 12.

DR SMART; SM00130; LRR 12.

DR SMART; SM00130; LDLR 1.

DR PR05ITE; PS50026; G_PROTEIN_RECEP_F1_2; 1.

DR PR05ITE; PS50030; LDLRA_1; 6.

DR PR05ITE; PS50030; LDLRA_2; 11.

RW Leucine-rich repeat; Signal.

FUNDAL 1.

FUNDAL 1.

FUNDAL 1.

FUNDAL 1.

FUNDAL 1.

FUNDAL 1.

FALSE_NEG.

CHARL 1.

FALSE_NEG.

DR PR05ITE; PS50048; DLRA_2; 1.

DR PR05ITE; PS50048; DLRA_2; 1.

DR PR05ITE; PS50048; DLRA_2; 1.

FR FINDAL 1.

FUNDAL 1.

FUNDA
                SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. SIMILARITY: CONTAINS 12 LDL-RECEPTOR CLASS A DOMAINS. SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
G-PROTEIN COUPLED RECEPTOR GRL101.
EXTRACELLULAR (POTENTIAL).
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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P02800;
1-101-1986 (Rel. 01, Created)
01-10V-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mctallothionein TA (MT-1A).
Beques caballus (Horse).
Euwaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      E9BB01297ECE356C CRC64;
LRR 6.
LRR 7.
BY SIMILARITY.
V SIMILARITY.
TMILARITY.
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Pred. No. 34;
3; Mismatches
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                               411 KSCLSGHCIEEHKWCNFHREC 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.3%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      125865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
TISSUE-Liver, and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 38.1
Matches 8; Conservative
      AA;
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SUBUNIT: MONOMER.

DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
POUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eukaryota: Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                           PROTEINS ARE
                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WT21_MYTED STANDARD; PRT; 71 AA.
P80251; P80257;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metallothionein 20-I isoforms A and B (MT-20-IB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48.5; DB 1; Length 61;
Pred. No. 5.7;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G -> R.
S -> L.
2E1B6EE3107C7353 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIMIS: PRO0860; MTVERTEBRATE.
PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
Metal-binding; Metal-thiolate cluster; Acetylation.
DOMAIN
1 29 BETA.
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InterPro; IPR000006; Metllthion_vert.
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                                               Trends Biochem. Sci. 3:90-93(1978).
                                                                                             REVISION TO 60, AND VARIANT ARG-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA
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Pfam; PF00131; metalthio; 1
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Best Local Similarity 34.v.
9; Conservative
Kojima Y., Kaegi J.H.R.;
"Metallothionein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A03277; SMH01A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P02795; 1MHU
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MT21_MYTED
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                                                                                                                                                                                                                              -i- INDUCTION: BY CADMIUM.
-i- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- INDUCTION: BY CADMIUM.
-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Digestive gland;
MEDIATE-9920055; PubMed-10190057;
BARSYLE D., White K.N., Lovejoy D.A.;
"Cloning and characterization of metallothionein cDNAs in the mussel
                                                                                                                   "Complete amino acid sequences of five dimeric and four monomeric forms of metallothionein from the edible mussel Mytilus edulis."; Eur. J. Blochem. 218:183-194(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E., Kaegl J.H.R., Fothergill J.E.; Complete amino acid sequences of five dimeric and four monomeric forms of metallothionein from the edible mussel Mytilus edulis."; Eur. J. Biochem. 218:183-194(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                     Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
Kaegi J.H.R., Fothergill J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mytilus edulis L. digestive gland.";
Comp. Biochem. Physiol. 122C:287-296(1999).
-!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
SEQUESTRATION OF TOXIC METAL IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                              66 66 S -> A (IN MT-20-IB).
71 AA; 6944 MW; 4FD275FE34E81654 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                           Metal-binding; Metal-thiolate cluster; Cadmium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metallothionein 20-II (MT-20-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%; Score 48.5; 40.7%; Pred. No. 6.
                                                                                                                                                                                             SEQUESTRATION OF TOXIC METAL IONS
                                                                                                                                                                                                                                                              PIR; S39420; S39420.
InterPro, IPR003019; Metallthion.
InterPro, IPR001008; Mtllthion_mlsc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NC-----CNGGCSSKWCR--DHARC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 NCIETNVCICGTGCSGKCCRCGDACKC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94062828; PubMed=8243463;
                                                                    MEDLINE=94062828; Pubmed=8243463;
 Mytiloidea; Mytilidae; Mytilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                    Pfam; PF00131; metalthio; 1. PRINTS; PR00875; MIMOLLUSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 40.7 nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                -!- SUBUNIT: HOMODIMER.
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15-JUN-2002 (Rel.
                  NCBI_TaxID=6550;
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P80252;
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                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: Secreted (By similarity).
-:- TISSUE SPECIFICITY: Expressed by the venom duct.
-:- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertides 20:1139-1144(1999).
-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Venom duct;

BEDILNE=20037955; PubMed=10573284;

Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;

*Conopeptides from Conus striatus and Conus textile by CDNA
                                                                                                                                                                           Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus textile (Cloth-of-gold cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 1; Length 76; Pred. No. 7.8;
                                                                                                                                                                                                          6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
B284206F1E149B4D CRC64;
                                                                                                                                               71 AA; 6887 MW; 4FD275FE39857654 CRC64;
                                                                                                                                                                              DB 1;
                                                                                     Pfan: PF00131; metalthio; 1.
PRINTS; PR00875; MTMOLLUSC.
Metal-binding; Metal-thiolate cluster; Cadmium.
                                                                                                                                                                                                                                                                                                                                                                         [6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                        Score 48.5; DE
                                                                                                                                                                                                                                                                                                                                              76 AA
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1; Mismatches
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BY SIMILARITY
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send an email to license@isb-sib.ch)
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                                           PIR; S39421; S39421.
InterPro; IPR003019; Metallthion.
InterPro; IPR001008; Mtllthion_mlsc.
                                                                                                                                                                                                                                       2 NC-----CNGGCSSKWCR--DHARC 19
                                                                                                                                                                                                                                                                                                                                                                                                                   Omega-type conotoxin TxO5 precursor
                                                                                                                                                                                                                                                                   5 NCIETNVCICGTGCSGKCCRCGDACKC 31
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
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                            EMBL; AJ005456; CAA06553.1; -.
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8582 MW;
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                                                                                                                                                                                             40.78;
                                                                                                                                                                                             Best Local Similarity 40.7
Matches 11; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001
15-JUN-2002
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CXO5_CONTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigations.";

Eur. J. Biochem. 267:7082-7093(2000).

Eur. J. Biochem. 267:7082-7093(2000).

Fur. J. Biochem. 267:7082-7093(2000).

HYDROXYGLUTARYL-COA TO GLUTACONYL-COA. THIS IS A KEY STEP IN THE HYDROXYGLUTARYL-COA TO GLUTACONYL-COA. THIS IS A KEY STEP IN THE PERMENYATION OF GLUTANATE. IT IS ACTIVATED BY HGDC.

FERRENYATION OF GLUTANATE. IT IS ACTIVATED BY HGDC.

FORACTOR: BINDS A 4FE-4S CLUSTER, WIN AND RIBOFLAVIN. REQUIRES ATP, MAGNESIUM AND A REDUCING AGENT, SUCH AS TI(III)CITRATE, FOR
 Gaps
                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Clostridia; Clostridiales; Acidaminococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hans M., Buckel W., Bill E.; "The iron-sulfur clusters in 2-hydroxyglutaryl-CoA dehydratase from The iron-sulfur clusters in 8-hydroxyglutaryl-CoA dehydratase from Acidaminococcus fermentans. Biochemical and spectroscopic
                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
(R)-2-hydroxyglutaryl-CoA dehydratase alpha-subunit (BC 4.2.1.-).
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                                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE—89276363; PubMed=2659350;
Dutscho R., Wohlfarth G., Buckel P., Buckel W.;
Cloning and sequencing of the genes of 2-hydoxyglutaryl-CoA dehydratase from Acidaminococcus fermentans.";
Eur. J. Blochem. 181:741-746(1989).
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-33.
MEDILNE=88082776; PubMed=3691501;
Schweiget G., Dutscho R., Buckel W.;
Purification of 2-hydroxyglutaryl-CoA dehydratase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 P -> A (IN REF. 2).
53890 MW; B7401C75EB7C4189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acidaminococcus fermentans. An iron-sulfur protein.";
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1; Mismatches
                                                                                                                                                               476 AA.
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   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 169:441-448(1987).
                                                                                                                                                                   PRT;
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   5;
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                                                                                                                                                                                                                                                                                            Acidaminococcus fermentans.
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     Conservative
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                                       1 ZNCCNGGCSSKWC 13
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Best Local Similarity
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63 QNCCDATCVVFWC 75
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=ATCC 25085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                              Acidaminococcus.
NCBI_TaxID=905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVITY
                                                                                                                                                                 HGDA_ACIFE
P11569;
     : 9
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                    HGDA_ACIFE
       Matches
                                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- INDUCTION: BY ADDITION OF L-AMINO ACIDS AFTER NITROGEN STARVATION, BY STARVATION IN PHOSPHATE BUFFER AND BY THE ADDITION OF PROTEIN SYNTHESIS INHIBITORS, D-AMINO ACIDS, OR ATP.
                                                                                                                                                                                                                                                                                                                                                                                   crassa.";
J. Biol. Chem. 265:17246-17251(1990).
-!- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                 MEDLINE-91009158; PubMed=2145270; Niedermann D.M., Lerch K.; "Molecular cloning of the L-amino-acid oxidase gene from Neurospora
                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mu-conotoxin PilitA precursor (Fragment).
Eukaryota, Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.8%; Score 48; DB 1; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAD (ADP PART) (POTENTIAL). 4B93DBBFA354B254 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
L-amino acid oxidase precursor (EC 1.4.3.2) (LAO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-AMINO ACID OXIDASE.
                                                                                                              695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A38314; A38314.
InterPro; IPR002937; Amino_oxidase.
Pfam; PF01593; Amino_oxidase; 1.
Oxidoreductase; Flavoprotein; FAD; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J05621; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76882 MW;
                  44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 ENVOSGGCISAWSRANGR 105
3 CCNG--GCSSKWCRDHAR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ZNCCNGGCSSKWCRDHAR 18
                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    + NH(3) + H(2)O(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         695 AA;
                                                                                                                                                                                                                                                                                                                     STRAIN=74-OR23-1A;
                                                                                                                                                                                                                            Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - COFACTOR: FAD
                                                                                                              OXLA_NEUCR
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P58925:
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SEQUENCE
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                                                                                                                             P23623
                                                                                             OXLA_NEUCR
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                                                                            RESULT 12
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M. Nielsen K.J., Watson M., Adams D.J., Hammarstroem A.K., Gage P.W.,
M. Nielsen K.J., Watson M., Adams D.J., Hammarstroem A.K., Gage P.W.,
M. Hill J.M., Craik D.J., Thomas L., Adams D., Alewood P.F., Lewis R.J.;
T. "Solution structure of mu-conotoxin PIIIA, a preferential inhibitor of
T. "Dersistent TIX-sensitive sodium channels.";
T. "Dersistent TIX-sensitive sodium channels.";
T. "Biol. Chem. 277:0-0(2002).
T. "FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
C. "FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
C. "FUNCTION: Mu-conotoxins bind and block voltage-sensitive and
fish. It blocks reversibly amphibian muscle Na+ channels (Probable).
T. SURGILLUAR LOCATION: Secreted.
T. SURGILLUAR LOCATION: Secreted.
T. TISSUE SPECIFICITY: Expressed by the venom duct.
T. TISSUE SPECIFICITY: Expressed by the venom duct.
T. TISSUE SPECIFICITY: Expressed by the venom duct.
T. SURGILLARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxin: Neurotoxin; Sodium channel inhibitor; Hydroxylation; Amidation; Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R->A: DECREASE IN AFFINITY TO CHANNEL FOE19F45BC97AC13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION (G-26 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                             Safo P., Rosenbaum T., Shcherbatko A., Choi D.-Y., Han E., Toledo-Aral J.J., Olivera B.M., Brehm P., Mandel G.; Distriction among neuronal subtypes of voltage-activated sodium channels by mu-concloxin PIIIA."; J. Neurosci. 20:76-80(2000).
                                                  Shon K.-J., Olivera B.M., Watkins M., Jacobsen R.B., Gray W.R., Floresca C.Z., Cruz L.J., Hillyard D.R., Brink A., Terlau H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠,
ش
                                                                                                    "mu-Conotoxin PIIIA, a new peptide for discriminating among
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UON-2002 (Rel. 41, Last annotation update)
Potential cadmium/zinc-transporting ATPase 2 (EC 3.6.3.3)
(EC 3.6.3.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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و
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   SEQUENCE FROM N.A., SYNTHESIS, AND MUTAGENESIS.
                                                                                                                         tetrodotoxin-sensitive Ņa channel subtypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROBABLE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROBABLE
                                                                                                                                                                             BINDING TO NEURONAL SODIUM CHANNELS.
                                                                                                                                            Neurosci. 18:4473-4481(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMA4 OR AT2G19110 OR T20K24.12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.0%;
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19
24
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                  TISSUE=Venom duct;
PubMed=9614224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 AA;
                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR.
PubMed=12006587;
                                                                                                                                                                                                  PubMed=10627583;
                                                                                       Yoshikami D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AHM2_ARATH
064474;
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R EMBL, AC002392, AAD12041.1.

R InterPro; IPR001756; Cu_ATPase.

InterPro; IPR001956; Cu_ATPase.

InterPro; IPR001956; Cu_ATPase.

R InterPro; IPR001954; Hlqnase/hydrlase.

R Pfam; PF00702; Hydrolase; 1.

R Pfam; PF00702; Hydrolase; 1.

R PROSTE; PR0019; CATATPASE.

R PROSTE; PS01047; HWA_1; FALSE_NEG.

R PHYCLASS—MEMBL PALSE_NEG.

R Hydrolase; Transmembrane; Phosphorylation; ATP-binding; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALYTIC ACTIVITY: ATP + H(2)O + Zn(2+)(In) = ADP + phosphate +
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=106.7. Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 402:761-768(1999).
-!- FUNCTION: INVOLVED IN CADMIUM/ZINC TRANSPORT (POTENTIAL).
-!- CATALYTIC ACTIVITY: ATP + H(2)0 + Cd(2+)(In) = ADP + phosphate
                                                                                SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA: TISSUE-ROOT; KITJGER G.C., BACCATILL P.J., Williams L.E.; Identification of AtHMA4, a putative heavy metal P-type ATPase in
                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMTLARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IB.
-i- SIMILARITY: CONTAINS I HMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                             Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL).
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cd(2+)(Out).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zn(2+)(Out)
                                                                                                                                                                 Arabidopsis."
                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
DOMAIN
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WAP 1..
WAP 2.
TRYPSIN INHIBITORY SITE (PROBABLE).
                                                                                                                                                                                        5; Indels 11;
                                                            PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                     DB 1; Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- INDUCTION: BY ESTROGEN AND PROGESTERONE; IN UTERUS.
-i- PTM: COMPARED TO HUMAN ALP, IT SEEMS TO LACK A CLEAVABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELASTASE INHIBITORY DOMAIN
                                                                                                                    1E913B9450443440 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRYPSIN INHIBITORY DOMAIN
                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL PEPTIDE.
                                                                                                                                                     35.4%; Score 47.5; L
36.7%; Pred. No. 71;
tive 3; Mismatches
                                                                                                                                                                                                                                                             1119 ETCCKVKIPEACASK-CRDRAKRHSGKSCC 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART: SM00217; WAP; 2. PROSITE; PS00317; 4_DISULFIDE_CORE; 2. Serine protease inhibitor; Repeat.
                                                                                                                                                                                                                           1 ZNCCN----GGCSSKWCRDHAR-----CC 20
 POTENTIAL
                                                   POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91155942; PubMed-2293019;
                                                                                                                      127208 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00003; 4DISULPHCORE.
ProDom; PD001224; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M57446; AAA63446.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A36113; A36113.
HSSP; P19957; 2REL.
Interpro; IPR002221; WAP.
Pfam; PF00095; wap; 2.
                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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114
59
113
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 700
1172
84
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401
601
605
681 701
701 117
18 1157 116
401 401
601 60
605 6C
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Antileukoproteinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
14
68
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GESTATION.
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                     ALK1_PIG
P22298;
 TRANSMEM
DOMAIN
                                                      DOMAIN
MOD_RES
METAL
                                                                                                                          SEQUENCE
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                                      DOMAIN
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                        ALK1_PIG
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2;
ELASTASE OR CHYMOTRYPSIN INHIBITORY SITE
BY SIMILARITY.
                                                                                                                                 7; Indels 18; Gaps
                                                                                                             Query Match 35.1%; Score 47; DB 1; Length 115; Best Local Similarity 26.3%; Pred. No. 14; Matches 10; Conservative 3; Mismatches 7; Indels
                                                                                                                                                 47 BY
51 BY
46 BY
55 BY
101 BY
105 BY
109 BY
12518 MW;
                  18
26
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88
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115 AA;
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Search completed: January 10, 2003, 08:32:59
Job time : 4.30435 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 10, 2003, 08:32:32; Search time 12 Seconds Run on:

(without alignments)
343.412 Million cell updates/sec

US-09-910-009A-432 Title: Perfect score:

134 1 ZNCCNGGCSSKWCRDHARCC 20 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* Database :

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mnc:*
sp_organele:*
sp_organele:* sp_unclassified:* SP_plant:*
SP_rodent:*
SP_virus:*
SP_vertebrate:* sp_rvirus:*
sp_bacteriap:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

		Description	11 1 2 1 m 2 m 2 5 5 5 5 C	Office arehidomic			O843h3 Oryza sativ				Obtes analysis	Obrige Series	Caycoo aeropyrum p	SOZZZO MUSCULU	The series of th	Ogno10 min saplen	Object 5 Hids Hidscull	20wsws certanymena Q14564 homo sapien	
	5	77	626060	O9FWK1	091,749	O9FEF3	08W3B3	081811	O9SRT7	O94KTR	OGREDS	097760	062220	064507	094092	ORVETG	ORWSW3	014564	
	a	9 ;	11	10	10	10	10	10	10	10		17	1	1	4	7,	'n	4	
	Query Match Length DB	Total Cit	199	404	442	550	188	362	452	456	48	258	223	230	410	875	162	169	
æ	Query		43.3	41.8	41.8	41.4	40.3	40.3	40.3	40.3	39.9	39.9	39.6	39.6	39.2	39.2	38.8	38.8	
	Score		58	26	99	55.5	54	54	54	54	53.5	53.5	53	53	52.5	52.5	52	52	
	Result No.		П	7	e	4	2	9	7	80	6	10	11	12	13	14	15	16	

Q94jb5 oryza sativ Q9vr08 drosophila Q9y7v5 trichoderma Q5225 mus musculu Q96874 ortanocha h	004500 arabidopsis 09x5b7 clostridium 09elt7 avian infec 077619 sus scrofa	U9444 CATLOROMUS Q899A9 brachydanio Q854x9 oryza sativ Q9/769 homo sapien Q9/1/17 lisishmanien	6 9		095syl caenorhabdi 08wqq3 calliphora 017641 caenorhabdi 0907t5 arabidopsis 067467 feline rota 022499 zea mays (m
Q94JB5 Q9VR08 Q9Y7V5 Q55225 Q96874			-	Q90WM1 Q9ST61 Q9XVX3 Q22048	0950Y1 08W003 017641 09C7T5 067467
10 5 3 11	10 12 12 6	113	10 12 2 2 5	113	5 10 10
1164 3680 1245 2910 231	454 480 539 801	621 122 367 389	462 78 115 167 271	353 466 152 164	185 197 404 491 493
38.8 38.8 38.4 38.4	388.1.2	37.7 37.3 37.3 37.3	37.3 36.6 36.6 36.6	36.6 36.2 36.2	36.2 36.2 36.2 36.2 36.2
52 52 51.5 51.5	51111	50.5 50 50 50	00 4 4 4 6 9 9 9 9	4 4 8 4 4 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	
17 18 19 20 21	22 23 24 25	22 28 30 30	31 32 34 35	36 33 30 30 30 30 30	14444 0 1

ALIGNMENTS

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clone: P0688A04.
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01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2000 (TrEMBLrel. 19, Last annotation update)
01-Dbc-2001 (TrEMBLrel. 19, Last annotation update)
Phytochelatin synthetase-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids III, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA;

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

Lin X., Kaul S., Town C.D., White O., Nierman W.C., Fraser C.M.;

Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;

"Arabidopsis thaliana chromosome I BAC F21N10 genomic sequence.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC027033; AAG12670.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.; Submitted (NoV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.8%; Score 56; DB 10; Length 404; 56.2%; Pred. No. 1.9;
                                                                              Score 58; DB 11; Length 199;
Pred, No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 404 AA; 45568 MW; 75D7A74D1BEF44AB CRC64;
 InterPro; IPR001368; TWFR_C6.
InterPro; IPR001007; VWF_C.
PR0517E; PS00525; TWFR_NGFR_1; UNKNOWN_1.
PR0517E; PS01208; VWFC; UNKNOWN_1.
SEQUENCE 199 AA; 23179 MW; 9074CCE116B56508 CRC64;
                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 AA.
                                                                                                                                                                                                                            404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-COLUMBIA;
MEDLINE-20363099; PubMed-10907853;
Nakamura Y.;
                                                                                                                                                                                                                             PRT;
                                                                                                                                                   1 ZNC---CNGGCSSK-WCRDHARCC 20
                                                                                                                                                                                                                                                                                             Hypothetical 45.6 kDa protein.
                                                                                 43.3%;
Local Similarity 41.7%;
hes 10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 NCCRGGVISAWAQDPA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NCCNGGCSSKWCRDHA 17
                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                              eurosids II; Bra
NCBI_TaxID=3702;
                                                                                      Query Match
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"Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1,
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Pred. No. 2.9;
2; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. NIPPOWBARE;
STRAIN=CV. NIPPOWBARE;
STRAIN=CV. NIPPOWBARE;
STRAIN=CV. NIPPOWBARE;
STRAIN=CV. NIPPOWBARE;
STRAIN=CV. Matsumoto T., Yamamoto K.;
Subaki T., Matsumoto T., Yamamoto K.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002783; BAB19098-1;
EMBL; AP002744; BAB19077-1;
SEQUENCE 550 AA; 60263 MW; IDE6FIBBABB9E8A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=CV. NIPPONBARE; Sasaki I., Matsumoto T., Yamamoto K.; Sasaki I., Matsumoto T., Yamamoto K.; Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                    Score 56; DB 10; Length 442; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   DNA Res. 77:217-221(2000).
EMBL; AP000736; BAB02996.1; -
SEQUENCE 442 AA; 49746 MW; 0D339878FC5D7E62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
putative zinc finger protein.
0SJNBA0013008.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
1-MAR-2001 (TrEMBLrel. 19, Last annotation update)
1-MAR-2001 (TrEMBLrel. 19, Last annotation update)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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52.9%;
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56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 NCCRGGVISAWAQDPA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 NCCNGGCSSKWCRDHA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
' Local 9; Conserva
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SEQUENCE FROM N.A.
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                                                                                                                                TAC and BAC clones.
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Matches 9; Conserv
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F14P3.14 protein.
F14P3.14.
                                                                                        NCBI_TaxID=3702;
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Q94KT8
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           Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansbarger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanaken S.E., Utterback T.R., Felalyum T.V., Kalb E., Quackenbush J., Salzberg S.L., White O., Fraser C.M.;

"Oryza sativa chromosome 3 BAC OSJNBa0013008 genomic sequence.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC084762; AAL58233.1;

InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        List RROW N.A.

Leuchter R., Wolf K., Zimmermann M.;

Leuchter R., Wolf K., Zimmermann M.;

"Isolation of an Arabidopsis cDNA complementing a Schizosaccharomyces pombe mutant deficient in Phytochelatin Synthesis (Accession No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned Pl clones.";

DNA Res. 4:401-414(1997).

EMBL; AJ006787; CAA07251.1;

EMBL; AB008269; BAB10641.1;

SEQUENCE 362 AA; 40321 MW; 2F6FBA72E7C68A93 CRC64;
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98162728; PubMed-9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima
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                                                                                                                                                                               Score 54; DB 10; Length 188;
Pred. No. 1.9;
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                                                                                                                                           PROSITE; PS50089; ZF_RING_2; 1.
SEQUENCE 188 AA; 19800 MW; 446FA90BE362A00B CRC64;
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                                                                                                                                                                                                                                                                                                                    362 AA.
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                    SMART; SM00184; RING; 1.
                                                                                                                                                                                                         Conservative
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94 HGGCLEKWLRAHGTC 108
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STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                              5 NGGCSSKWCRDHARC
                                                                                                                                                                   Query Match
Best Local Similarity
1.25 8; Conservē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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081811;
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Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schindelman G., Morikami A., Jung J., Baskin T.I., Carpita N.C., Schindelman G., Morikami A., Jung J., Baskin T.I., Carpita N.C., Derbyshire P., McCann M.C., Benfey P.N.;
"COBRA encodes a putative GPI-anchored protein, which is polarly localized and necessary for oriented cell expansion in Arabidopsis."; Genes Dev. 115:1115-1127(2001).

EMBL: AF319663; AAK56072.1; ...
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                              STRAINCY. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Roning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F14P3 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC009755; AAR02128.1;
SEQUENCE 452 AA; 50363 MW; Alal820E0AF96227 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 10; Length 452; 
Pred. No. 4;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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135 NCCRGGVLNSWAQDPA 150
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138 NCCKGGVMNSWVQDPA 153
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Matches 8; Conserv
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STRAIN-BALB/C
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                                                                                                                                                      Calcutt M.J. Lavrar J.L., Wise K.S.;

Calcutt M.J., Lavrar J.L., Wise K.S.;

"Is1630 of Mycoplasma fermentans, a novel IS30-type insertion element that targets and duplicates inverted repeats of variable length and sequence during insertion.";

J. Bacteriol. 181:7597-7607(1999).

EMBL, ART79376; AART5567.1;

SEQUENCE 48 AA. 5319 MM; 668836FA3592B2C7 CRC64;
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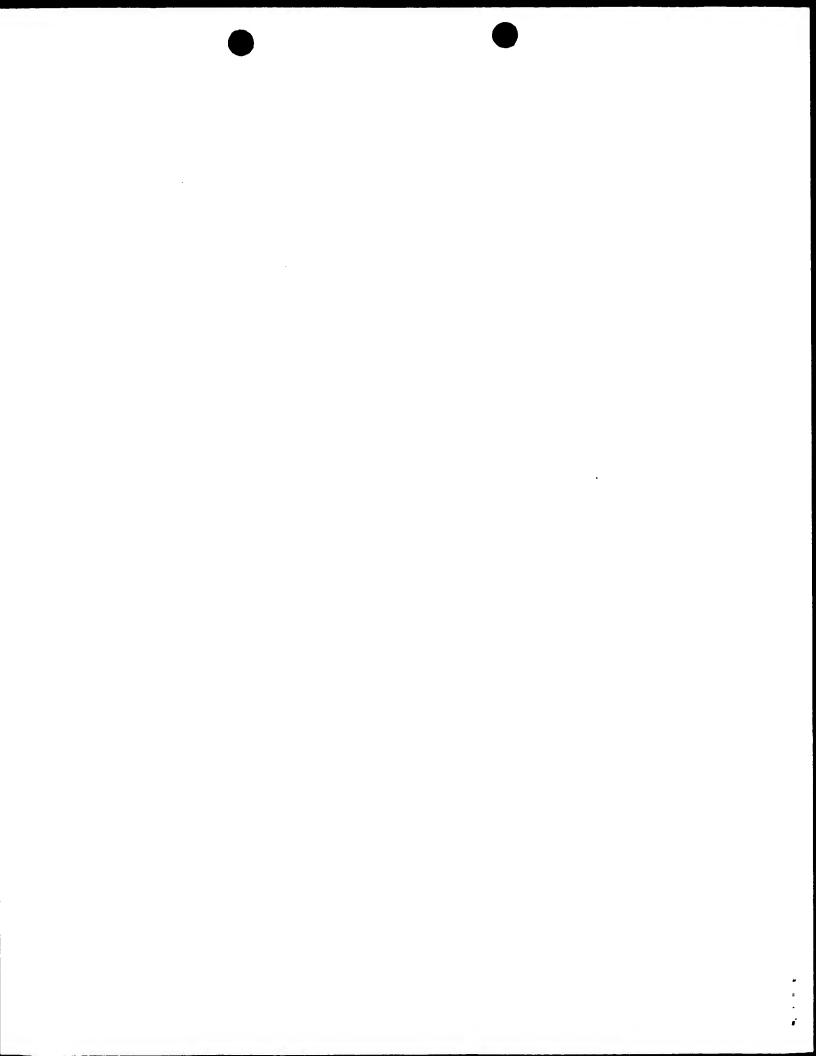
Kawarabayasi Y. Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Naqai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oquohi A., Aoki K.-I., Kubota K.,
Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                       Gaps
                                  MEDILINE—99115554; PubMed-9916088; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.; "Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans."; Infect. Immun. 67:760-771(1999).
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                                                                                                                                                                                                                                               Score 53.5; DB 2; Length 48; Pred. No. 0.69;
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Hypothetical protein; Complete proteome.
SEQUENCE 258 AA; 28713 MW; 25C2FDB73F178AEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein APE1391.
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                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                            MEDLINE=20069643; PubMed=10601219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desulfurococcaceae; Aeropyrum NCBI_TaxID=56636;
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Best Local Similarity 42.1.
Best Similarity 42.1.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aeropyrum pernix.
       [1]
SEQUENCE FROM N.A.
                                                                                                                        SEQUENCE FROM N.A.
                              STRAIN=PG18
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Q62220;
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Q9YC60
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STRAIN=BAIB/C;
MEDINDE=91154184; PubMed=1840598;
MEDINDE=91154184. Hatzenbuhler N., Vogeli G.;
Wood L., Mils M., Hatzenbuhler N., Vogeli G.;
Additions and Corrections: Serine-rich ultra high sulfur protein gene expression in murine hair and skin during the hair cycle.";
J. BAOL Chem. 266:4024-4024(1991).
EMBL: M37760; AAA40107.1;
HSSP; P01064; 1P12
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"Serine-rich ultra high sulfur protein gene expression in murine hair and skin during the hair cycle.";
J. Biol. Chem. 265:21375-21380(1990).
EMBL: M37759; AA40106.1; -.
HSSP; P01064; 1P12.
                                                                                                                                                                                                                                                                                                                                                                                            Wood L., Mills M., Hatzenbuhler N., Vogeli G.; "Serine-rich ultra high sulfur protein gene expression in murine hair and skin during the hair cycle."; J. Biol. Chem. 265:21375-21380(1990).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C654BDB9FD08C59A CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
serine 2 ultra high sulfur protein.
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Interpro; IPR001450; 4Fe4S_ferredoxin.
Interpro; IPR0010020; Anaphylatoxin.
Interpro; IPR001305; DnaJ_CXXCXGXG.
Interpro; IPR001007; VWF_C.
Interpro; IPR001097; 4Fe4S_FERREDOXIN; UNKNOWN_I.
PROSITE; PS01177; ANAPHYLATOXIN_I; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOSCI, MGI.1354786; Krtap5-4.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001007; VWF_C.
PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_2.
PROSITE; PS01208; VWFC; UNKNOWN_2.
SEQUENCE 223 AA; 21442 MW; C654BDB9FD08C59.
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MEDLINE=91065960; PubMed=2250030;
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91065960; PubMed=2250030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 CCSSGCGSSCCQ--SSCC 174
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Best Local Similarity
8; Conserva
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 45.9 kDa protein (Unknown) (Protein for MGC:4732).
DKF2P434J087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.2%; Score 52.5; DB 4; Length 410; 47.6%; Pred. No. 6.1;
                                                   39.6%; Score 53; DB 11; Length 230; 44.4%; Pred. No. 3.1;
                                                                              Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL. BC020002; AAH20002.1; -.
InterPro; IPR01680; WD40.
Pfam; PF00400; WD40; 4.
Bypothetical protein.
SEQUENCE 875 AA; 98322 MW; 1A5C40C907F7533B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-LUNG;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL138(892; CAB66826.1; -.
EMBL; BC005883; AAH05883.1; -.
PROSITE; PS00637; DNAJ_CXXCXGXG; UNKNOWN_1.
PROSITE; PS01208; VWFC; UNKNOWN_3.
SEQUENCE 230 AA; 21781 MW; 6CC50B41B2137C23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 410 AA; 45862 MW; C6ACC5CD0883C5D2 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein.
Mus musculus (Mouse)
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                                                                            3; Mismatches
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                                                               44.48;
                                                                                                                   120 CCSSGCGSSCCQ--SSCC 135
                                                                                                    3 CCNGGCSSKWCRDHARCC 20
                                                                            Conservative
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                                                                                                                                                                                             PRELIMINARY;
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                                                   Query Match
Best Local Similarity
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Q8VE19;
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Q8VE19
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Gorovsky M.A.;
A Robust Inducible-Repressible Promoter Greatly Facilitates Gene
Knockouts, Conditional Expression and Overexpression of Homologous and
Heterologous Genes in Tetrahymena thermophila.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY061892; AAL31645.1;
SEQUENCE 162 AA, 16757 MW; 9B2DB3C95981FFCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
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9
         DB 11; Length 875;
                                                      Indels
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Metallothionein.
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39.2%; Score 52.5; Di
47.6%; Pred. No. 12;
tive 2; Mismatches
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Job time: 14 secs
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                                                                                             2 NCCNGGCSS---KWCRDHARC 19
  Query Match 39.2
Best Local Similarity 47.6
Matches 10; Conservative
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                                                                                                                                                                                                                   RESULT 15
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 10, 2003, 08:32:32; Search time 5.91304 Seconds Run on:

(without alignments)
99.519 Million cell updates/sec

US-09-910-009A-432 Title:

1 ZNCCNGGCSSKWCRDHARCC 20 Perfect score: :eduence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

262574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*

!: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
?: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
?: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
!: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
?: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
?: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Segment of account of the segment of	Sequence 1, Appli	7,4	Sequence 23. Appl	23	Sequence 14. Appl	16.		Patent No. 5223423	12. App	13	٠.	1	ì	į (Sequence 12 appl	1 -	Sequence 26 Appli	4 2	, v	0	23	, ,	ì	Sequence 53 April	4	Sequence 4, Appli
SUMMARIES	ID	US-08-900-230-3	-60-	õ	US-08-279-058B-23	-08-828-323-2	US-09-003-198A-14	US-09-003-198A-16	US-08-977-767-3	5223423-3	US-09-314-242-12	US-09-548-372D-13	US-09-548-367D-13	US-08-599-556-1	PCT-US96-05262-2	US-08-599-556-7	PCT-US96-05262-12		US-08-975-080-26	US-08-691-814B-42	S	US-08-836-134-23	US-09-493-784-23	6-134-	-493-784	-08-900-230-	-07-668-648-	US-08-429-998-4
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ф	Query Match	42.5	41.8	39.5	38.8	38.8	38.1	38.1	37.7	36.6	35.8	35.8	35.8	35.4	35.4	35.4	35.4	35.4	35.1	35.1	35.1	35.1	35.1	35.1	35.1	34.7		34.7
	Score	57	26	52.5	25	52	51	51	50.5	49	48	48		7	7	7	47.5	7	47	47	47	47	47	47	47		46.5	9
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Sequence 4, Appli		Sequence 4, Appli		Sequence 17. Appl	40,	, ,		ì	Sequence 5. Appli	4		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		Α	Sequence 22 Appl	Sequence 9, Appli
US-08-431-333-4	US-186-991-862-1/	IS-09-227-357-579	US-08-761-248B-11	US-08-239-256-17	US-08-900-230-40	US-08-527-044-2	US-09-013-780-2	US-07-906-349A-6	US-08-872-855-5	US-08-872-855-4	US-08-981-392-12	US-08-390-882A-1	US-08-390-882A-2	US-08-900-230-46	US-08-508-761B-22	US-08-460-529B-9
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34.7	7. 4.	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.0	34.0	34.0	33.6	33.6	33.6	33.6	33.6
46.5	4.0	46	46	46	46	46	46	46	45.5	45.5	45.5	45	45	45	45	4 5
28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Bard, Jonathan A.
TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
TELECOMMUNICATION INFORMATION:
TELEPHONIC: 212-278-0400
TELEPAX: 212-391-0525
                                                                                                                                                                                                       ADDRESSEE: Cooper & Dunham LLp
STREET: 1185 Avenue of The Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/900,230 FILING DATE: 23-UUL-1997 FLLASIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                        ; Sequence 3, Application US/08900230
; Patent No. 6329197
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: pc-nocare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1417 amino acids
                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: U.S.A.
ZIP: 11036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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STRANDEDNESS: sin
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                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                  New York
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US-08-900-230-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
RESULT 1
US-08-900-230-3
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540 CCTGGCCGTGCGCCACCC 557 3 CCNGGCSSKWCRDHARCC 20 qq ò

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Gaps

; 0

Score 57; DB 4; Length 1417; Pred. No. 45; 0; Mismatches 9; Indels

42.5%; 50.0%;

Query Match Best Local Similarity

9; Conservative

Matches

2

single

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STRANDEDNESS:
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APPLICANT: HOFFWAN, NO. 6309820h
APPLICANT: HOFFWAN, NO. 6309820h
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
APPLICANT: MCCONNELL, Stephen J.
APPLICANT: DIVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
                                                                                                                                            GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000849
CURRENT APPLICATION NUMBER: US/09/738,884
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.8%; Score 56; DB 4; Length 2211; 50.0%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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....ER: US/08/630,915A
03-APR-1996
N: 536
TNN: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/08630915A Patent No. 6309820 GENERAL INFORMATION:
                                                                                                 ; Sequence 1, Application US/09738884 ; Patent No. 6391606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 1036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1400 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CCNGGCSSKWCRDHARCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.07
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Human
US-09-738-884-1
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ZIP: 1003
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
LENGTH: 2211
                                                           RESULT 2
US-09-738-884-1
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Gaps
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                                                                    39.2%; Score 52.5; DB 4; Length 1400; 50.0%; Pred. No. 1.4e+02; Live 1; Mismatches 5; Indels 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: O'Donnell, Michael
TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME
FILE REFERENCE: 19603/10214
CURRENT APPLICATION NUMBER: US/08/828,323A
CURRENT FILING DATE: 1997-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRF D-1056CIP
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Michael B. O'Donnell
TITLE OF INVENTION: DNA POLYMERASE III
TITLE OF INVENTION: HOLOENZYME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/279,058B
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                                                                                                                                                                                                                                                                                   US-08-279-058B-23
Sequence 23, Application US/08279058B
; Patent No. 5668004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REPERENCE/DOCKET NUMBER: CRF I
TELECOMMUNICATION INFORMATION:
TELEFAX: (203)268-1951
TELEFAX: (203)268-1951
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Word 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                         190 CCGGGCA---CTGTACCC 204
                                                                                                                                                            3 CCNGGCSSKWCRDHARCC 20
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                                                                               Query Match 39.2;
Best Local Similarity 50.0;
Matches 9; Conservative
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Best Local Similarity
TOPOLOGY: linear MOLECULE TYPE: DNA
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US-08-828-323-23
                       ; MOLECULE TYP:
US-08-630-915A-37
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ligary, Jihong
APPLICANT: Ligary, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Way Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold White & Durkee
                                                                                                                                      Score 52; DB 4; Length 58;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.1%; Score 51; DB 4; Length 40; 40.7%; Pred. No. 10; 6; Indels tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/003,198A FILING DATE: 07-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09003198A Patent No. 6316407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 16, Application US/09003198A
                                                                                                                                        38.8%;
milarity 47.1%;
Conservative
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NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 58
                                                                                                                                                                                                                4 CNGGCSSKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.7<sup>3</sup>
Matches 11; Conservative
                                                                                     ; ORGANISM: Escherichia coli
US-08-828-323-23
                                                                                                                                                                                                                                                38 CTGGCTACTCGTGAACC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. Box 4433 CITY: Houston
                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
US-09-003-198A-14
                                                                                                                                                                                                                                                                                                                      US-09-003-198A-14
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US-09-003-198A-16
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                                                                        TYPE: PRT
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Gaps
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    APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.1%; Score 51; DB 4; Length 67; 40.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: DOS
FastSEQ for Windows Version 2.0
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Patent No. 5972684
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Yue, Henry
APPLICANT: Greenwald, Sara
APPLICANT: Corley, Noil C.
TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 16;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               JMBER: US/09/003,198A
07-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: MOBT:193
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CNGGCS-----SKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 CFGCDFHCKTKEHLLSGRCRDDFRCC 67
                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              STATE.
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"TOTAL TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (713) 787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.1 Best Local Similarity 40.7 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                         STREET: P.O. Box 4433
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-003-198A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                             Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-977-767-3
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TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT

HUMINODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/331,212

FILING DATE: 03-31-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3025;
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Sequence 12, Application US/09314242A

Patent No. 6248575

GENERAL INFORMATION:
APPLICANT: Elizabeth J. Golightly
TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity
FILE REFERENCE: 5556, 200-US
CURRENT APPLICATION NUMBER: US/09/314, 242A

EARLIER APPLICATION NUMBER: 09/080, 428

EARLIER FILING DATE: 1998-05-18

MUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50.5; DB 2; Length 1 Pred. No. 2.2e+02; 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.6%; Score 49; DB 6; Length 302
38.9%; Pred. No. 6.5e+02;
tive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FRANCHINI, GENOVEFFA; WONG-STAAL, FLOSSIE;
                                                                                                                                                                              NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0423 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
CURRENT APPLICATION DATA:
                                APPLICATION NUMBER: US/08/FILING DATE: Herewith CLASSIFICATION: 424
PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.7%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1345 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             774 CCTGGCCATTC-TCAGCC 790
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Best Local Similarity 50.0*
                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           IMEDIAL
LIBRARY: General
1532042
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TITLE OF INVENTION: ALLEMEN'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
TITLE OF INVENTION: ALLEMENCE
TITLE OF TITLE OF ALLEMENCE: 29915/62801
CURRENT APPLICATION NUMBER: US 60/155,493
PRIOR PELING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1998-09-24
SOOTWARRE PRIOR NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
SOOTWARE: PAGENTION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
SOOTWARE: PAGENTION VERSION 3.1
SEQ ID NO 13
FENOR! APPLICATION VERSION 3.1
SEQ ID NO 13
FENOR! APPLICATION OF THE OWN APPLICA
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TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE COE INVENTION: THEREOF
FILE REPERENCE: 29915/6280H
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT PILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1999-09-24
SPRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATCHTIN OF: 73
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                                                                                                                                                                                                                                                                                                Length 695;
                                                                                                                                                                                                                                                                                            Score 48; DB 4; Length 695
Pred. No. 2.4e+02;
3; Mismatches 7; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ 1D NO 12
LENGTH: 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 13, Application US/09548372D
; Patent No. 6420534
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ilarity 44.4%;
Conservative
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88 ENVQSGGCISAWSRANGR 105
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Matches 8; Conserve
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Matches 8; Conserv
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GENERAL INFORMATION:
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                                                                                                                                          TYPE: PRT
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STRANDEDNESS: single
TOPOLOGY: linear
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           LOCATION:
                                             NAME/KEY:
                                                               LOCATION:
                                                                                               NAME/KEY:
                                                                                                                  LOCATION:
                                                                                                                                                    NAME/KEY:
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                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                     LOCATION
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APPLICANT: Yoshikami, Doju
APPLICANT: Yoshikami, Doju
APPLICANT: Cruz, Lourdes J.
APPLICANT: Glivera, Baldomero M.
TITLE OF INVENTION: Conotoxin Peptide PIIIA
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                         Length 2088;
                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,556
                                                                                                         35.8%; Score 48; DB 4; 344.4%; Pred. No. 6.2e+02;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 24260-107674-03
TELECOMUNICATION INPORMATION:
TELEPHONE: 202-965-4848
TELEFAX: 202-962-8300
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                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08599556
Patent No. 5670622
GENERAL INFORMATION:
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ORGANISM: Conus purpurascens
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COMPUTER: IBM PC compatible
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                                                                                                                                                                                                               1617 CCTGGACGATCTCCAGCC 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               3 CCNGGCSSKWCRDHARCC 20
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                                                                                                                        Best Local Similarity 44.4

Autches 8; Conservative
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LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Saxe, Stephen A. REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-13
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OTHER INFORMATION:
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SEQ ID NO 13
LENGTH: 2088
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CITY: Wa
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                                                                                                                                                                                                                                                                     RESULT 13
US-08-599-556-1
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                                                                                                           Query Match
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/note= "Amino acid 18 is 4-transhydroxyproline or proline.
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/note= "The carboxy terminus may be amidated."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05262
                                                                                                                                                                                                                                                                                                                                                                                                                               .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9605262
GENERAL INFORMATION:
APPLICANT: Shon, Ki-Joon
APPLICANT: GIIlley, Michelle M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Voshikami, Doju
APPLICANT: Tuz, Lourdes J.
APPLICANT: Tuz, Lourdes J.
APPLICANT: Hillyard, David R.
TITLE OF INVENTION: Conotoxin Peptides
                                                                                                                                                                                                  /product= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24260-107674
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17-APR-1996
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APPLICATION NUMBER: US 08/423,561
FILING DATE: 17.APR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38,609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CCGFXKSCRSRQCKXH-RCC 22
                                    Disulfide-bond
                                                                                             Disulfide-bond
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                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
                                                                                                                                                       Modified-site
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202-962-8300
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Venable, F
                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
4..16
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3 CCN--GGCSSKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                  7 CCGFPKSCRSRQCKPH-RCC 25
 ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.04
                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-599-556-7
                                                                                                                                                                             amino acid
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /product- "OTHER" OTHER INFORMATION: /note= "Amino acid 18 is 4-trans-hydroxyproline or proline."
                                                                                                                                                                                                    7
                                                                                                                            OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Amino acid 1 is pyroglutamate or glutamine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "OTHER"
/note= "The carboxy terminus may be amidated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Yoshikami, Doju
APPLICANT: Warsh, Maren
APPLICANT: Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Conoctoxin Peptide PIIIA
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08599556 Patent No. 5670622 GENERAL INFORMATION:
                                                                  ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CCN--GGCSSKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
5..21
                                                                                                                                                                                                                                                                Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
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                                                                                                  NAME/KEY: Modified-site
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Best Local Similarity 45.0'
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005-3917
COMPUTER READABLE FORM:
: peptide
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION:
CTHER INFORMATION:
PCT-US96-05262-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                 ORIGINAL SOURCE:
              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
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LOCATION:
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LOCATION:
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                                                                                                                     LOCATION:
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US-08-599-556-7
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3; Gaps
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NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24260-107674-03
TELECOMMUNICATION INFORMATION:
TELEPAN: 202-962-4848
TELEPAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: January 10, 2003, 08:38:19 Job time : 6.91304 secs
```

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

January 10, 2003, 08:33:07; Search time 30.9565 Seconds (without alignments) 12.534 Million cell updates/sec Run on:

US-09-910-009A-432 Perfect score:

134 1 ZNCCNGGCSSKWCRDHARCC 20 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: 118974 seqs, 19401057 residues

118974

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

/cgn2_6/pcdata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

/cgn2_6/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*/cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*/cgn2_6/ptcdata/2/pubpaa/US10_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	* Query Match Length DB	DB	ID	Description
1	58	43.3	3907	6	US-10-029-217A-24	Lank AC Operations
7	26	41.8	2211	6	US-10-096-961-1	Sequence 24, Appl
m	55	41.0	1497	10	US-09-060-854B-2	Sounded 1, Appli
4	53	39.6	32	10	US-09-894-882-470	Segmence Z, Appli
S	53	39.6	40	10	US-09-894-882-498	
9	53	39.6	68	10	US-09-894-882-274	Sequence 430, App
7	53	39.6	1200	10	US-00-826-508-3	Sequence 2/4, App
ω	52.5	39.5	1400	10	US-09-879-37	Sequence 3, Appli
σ	52.5	39.2	4679	10	US-09-804-898-2	Sognongo 3 , Appi
10	20	37.3	1743	12	US-10-052-586-451	Sequence 2, Appli
11	49	36.6	4.2	α	115-08-969-137-3	Sequence 451, App
12	49	36.6	1300	1,	IIS-10-052-586-260	Sequence 3, Appli
13	48	35.8	32		115-09-864-761-41000	Sequence 209, App
14	47	35.1	09	ι σ	118-09-796-692-1464	Sequence 41823, A
15	47	35.1	9	۱ ۵	TC-00-100-1001	Sequence 1494, Ap
9			000	, 5	US-03-730-037-1371	Sequence 1921, Ap
7 -	7	7.00	000,	7	US-U9-864-761-38546	Sequence 38546, A
À .	7"	1.00	1403	œ	US-08-913-322-22	Sequence 22, Appl
87	4/	35.1	1403	œ	US-08-913-322-24	Sequence 24. April
19	47	35.1	1422	10	US-09-735-933-1	Segmence 1 Appli

Sequence 17, Appl	17,	Sequence 1416. An	Sequence 19, Appl	Sequence 58, Appl	Sequence 105. App		Sequence 426. App	428		437	187	, ,	104	Segmence 27 Appl	Segmence 1361 an		Sequence 10 Appl	12,	, , ,		Sequence 16 Appl	182	, ,	Sequence 12, Appl
US-09-824-647-17 0 US-09-813-156-17	0 US-09-824-807-17	0 US-09-925-301-1416	0 US-09-894-882-19	0 US-09-894-882-58	0 US-09-894-882-105	0 US-09-894-882-407	0 US-09-894-882-426	0 US-09-894-882-428	0 US-09-894-882-28	0 US-09-894-882-431	0 US-09-894-882-18	0 US-09-894-882-57	0 US-09-894-882-104	0 US-09-894-882-27	0 US-09-925-300-1361	0 US-09-764-903-50	0 US-09-898-570-10	0 US-09-898-570-12	US-09-975-143-47	0 US-09-898-570-14	0 US-09-898-570-16	2 US-10-052-586-581	0 US-09-845-583-10	0 US-09-908-322-12
593 9 593 1	593 1	621 1	46 1	46 1	46 1	46 1	46 1	46 1	48 1	48	82	82 1	82 1	84 1	137	252	735 10	845 10	914 9	974 1(1009 10	1435 13	1587 10	722 1(
34.7	34.7	34.7	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.0
46.5	46.5	46.5	46	46	46	46	46	46	46	46	46	46		46	46	46	46	46	46	46	46	46	46	45.5
20 21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: OLSON, ERIC N.
APPLICANT: OLSON, ERIC N.
APPLICANT: OLSON, ERIC N.
APPLICANT: WANG, DA-ZHI
TITLE OF INVENTION: MUCLEAR REGULATORY FACTOR
TITLE OF INVENTION: NUCLEAR REGULATORY FACTOR
TITLE OF INVENTION: NUCLEAR REGULATORY FACTOR
TITLE OF INVENTION: NUMBER: USD.6950S
CURRENT APPLICATION NUMBER: USD.002-03-19
PRIOR APPLICATION NUMBER: 60/257,761
PRIOR PLING DATE: 2000-12-21
NUMBER OF SED ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 24
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB 9; Length 3907; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                 Sequence 24, Application US/10029217A Patent No. US20020164735A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mus musculus US-10-029-217A-24
RESULT 1
US-10-029-217A-24
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535 CCTGGCAGAGCAGCCTCC 552 3 CCNGGCSSKWCRDHARCC 20 qq δ

Sequence 1, Application US/10096961 Patent No. US20020155772A1 : GENERAL INFORMATION: APPLICANT: GUEGLER, Karl et al. RESULT 2 US-10-096-961-1

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE TITLE OF INVENTION: PROTEINS, AND USES THEREOF FLLE REPERENCE: CLOOO849DIV CURRENT APPLICATION NUMBER: US/10/096,961

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                                                                                                                                                                                                                                                                                                                                            39.6%; Score 53; DB 10; Length 32; 52.9%; Pred. No. 2.7; Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Generix, Inc.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Eslec
APPLICANT: Jimenez, Eslec
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watthin, Marten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WALLEL, WALELL
APPLICANT: Shen, Greg S.
TYTLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2001-01-29
NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 470
LENGTH: 32
TYPE: PRT
ORGANISM: Conus virgo
US-09-894-882-470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 274, Application US/09894882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 498, Application US/09894882; Patent No. US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.99
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CCNGGCSSKWCRDHARC 19
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Best Local Similarity 52.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Conus virgo US-09-894-882-498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-894-882-274
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APPLICANT: Estell, David Aaron
TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. US2002008
TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. US2002008
TITLE OF INVENTION: Proteins
FILE REPERBURE: GC532
CURRENT PAPLICATION NUMBER: US/09/060,854B
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1497
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                                                                                                                                                                                                                                                                                                                      41.8%; Score 56; DB 9; Length 2211; 50.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: I-Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                               PRIOR APPLICATION NUMBER: 60/232,632
PRIOR APPLICATION NUMBER: 00/732,632
PRIOR PILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-12-18
NUMBER OF SED ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 470, Application US/09894882; Patent No. US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09060854B; Patent No. US20020081703A1
                            CURRENT FILING DATE: 2002-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-09-060-854B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1017 CCTGGCGTATCT--ATCC 1032
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Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CCNGGCSSKWCRDHARCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 CCCGGCTCCGCAAGATCC 64
                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 50.00
Best Local 9, Conservative
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Matches 9; Conserva
                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Homo sapien US-10-096-961-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Watkins, APPLICANT: Jones, Re
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                                                                                                                                                                                                                     LENGTH: 2211
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                                                                                                                                                                                                  SEQ ID NO 1
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US-09-879-957-37
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
TITLE OF INVENTION: and Polynucleotides
FILE REFERENCE: GP-70744USB
CURRENT APPLICATION NUMBER: US/09/826,508
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 3.0
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                                      APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                          APPLICANT: Waterlas, water and APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION I-Superfamily Conotoxins FILE REFERENCE: 2010-06-29
PRIOR APPLICATION NUMBER: US 60/246,29
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-16-30
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-04
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PALENTIN VETSION 3.0
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.6%; Score 53; 52.9%; Pred. No.
                                                           APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: Mointosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
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Patent No. US20010025099A1
GENERAL INFORMATION:
APPLICANT: Nabil Elshourbagy
APPLICANT: Lisa Vawter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.6%;
44.4%;
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Best Local Similarity 52.5.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 44.4
Matches 8; Conservative
US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Conus virgo
US-09-894-882-274
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RESULT 8

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HOFEWARY, BIDDEN M.
KAY, BIDDEN M.
FOWLKES, Dana M.
MCCONNELL, Stephen J.
MCCONNELL, Stephen J.
DOCONNELL, STEPHED BY HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: DURING, MATTHEW
APPLICANT: XIAO, WEIDONG
TITLE OF HIVENTON: PRODUCTION OF CHIMERIC CAPSID VECTORS
FILE REFERENCE: 102182-14
CURRENT APPLICATION NUMBER: US/09/804,898
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/189,110
PROOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                              APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755Alh
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.2%; Score 52.5; C
50.0%; Pred. No. 58;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-879-957-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
Sequence 37, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1400 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 CCGGCCA---CTGTACCC 204
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                                                                                                                                                                                                                                                                                                                                               STATE: New York
                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                         Score 52.5; DB 10; Length 4679;
Pred. No. 1.5e+02;
2; Mismatches 3; Indels 5;
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CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR PEDLICATION NUMBER: 60/059263
PRIOR PELLING DATE: 1997-09-18
PRIOR PELLING DATE: 1997-09-18
PRIOR PELLING DATE: 1997-09-18
PRIOR PELLING DATE: 1997-09-18
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-24
PRIOR PELLING DATE: 1997-10-28
PRIOR PELLING DATE: 1997-10-29
PRIOR PELLING DATE: 1997-10-29
PRIOR PELLING DATE: 1997-10-29
PRIOR PELLING DATE: 1997-10-29
PRIOR PELLING DATE: 1997-10-39
PRIOR PELLING DATE: 1997-10-39
PRIOR PELLING DATE: 1997-10-31
PRIOR PELLING DATE: 1997-10-39
PRIOR PELLING DATE: 1997-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 451, Application US/10052586 Patent No. US20020127584A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
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APPLICATION NUMBER: 60/069335
FILING DATE: 1997-12-11
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PRIOR FILING DATE: 1997-111-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
                                                                               ; TYPE: PRT
; ORGANISM: adeno-associated virus 2
US-09-804-898-2
                                                                                                                                                                                 Ouery Match 39.2%;
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                          4621 CCGGGCTTTGC----CC 4633
SOFTWARE: PatentIn version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe, Colin K.
                                                                                                                                                                                                                                                                                            3 CCNGGCSSKWCRDHARCC 20
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Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-052-586-451
                                                         LENGTH: 4679
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PRIOR FILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR PILING DATE: 1998-04-22
PRIOR PLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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R APPLICATION NUMBER: 60/083496
R RFILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083499
R FILING DATE: 1998-04-29
R RAPLICATION NUMBER: 60/083559
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/084366
R FILING DATE: 1998-05-05
R APPLICATION DATE: 1998-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR APPLICATION NUMBER: 60/080333
DR FILING DATE: 1998-04-01
DR APPLICATION NUMBER: 60/081049
DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081070
DR FILING DATE: 1998-04-08
                                          R FILING DATE: 1997-12-17
R APPLICATION NUMBER: 60/068017
R FILING DATE: 1997-12-18
R APPLICATION NUMBER: 60/077450
R FILING DATE: 1998-03-10
R APPLICATION NUMBER: 60/077632
                                                                                                                                                                                                        R FILING DATE: 1998-03-11
R APPLICATION NUMBER: 60/077649
R FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/07886
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/078939
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FILLING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
                                                                                                                                                                                                                                                                                                                                                                                                     APFLING DATE: 1998-03-2/
APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/080107
APPLICATION NUMBER: 60/080107
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FILING DATE: 1998-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/085580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
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FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
FILING DATE: 1997-12-12
APPLICATION NUMBER: 60/069870
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/080194
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PRIOR APPLICATION NUMBER: 00/086486
PRIOR FILING DATE: 1998-05-22
PRIOR PLICATION NUMBER: 60/086486
PRIOR PLICATION NUMBER: 60/087098
PRIOR PLILOR DATE: 1998-05-28
PRIOR PLILOR DATE: 1998-05-28
PRIOR PLILOR DATE: 1998-05-28
PRIOR PLILOR DATE: 1998-05-28
PRIOR PLILOR DATE: 1998-06-02
PRIOR PLILOR DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08759
PRIOR PLILOR DATE: 1998-06-02
PRIOR PLILOR DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08025
PRIOR PLING DATE: 1998-06-04
PRIOR PLILOR DATE: 1998-06-04
PRIOR PLILOR DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
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PRIOR PLILOR DATE: 1998-06-04
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PRIOR PLILOR DATE: 1998-06-04
PRIOR PLILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08803
PRIOR APPLICATION NUMBER: 60/08803
R PILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/086023
R PILING DATE: 1998-05-18
R APPLICATION NUMBER: 60/086392
R FILING DATE: 1998-05-22
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088740
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088825
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APPLICATION NUMBER: 60/089090
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APPLICATION NUMBER: 60/088811
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER:
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GENERAL INFORMATION:
APPLICANT: KANDEL, ERIC
APPLICANT: MARK
TITLE OF INVENTION: DNA REGULATORY ELEMENT FOR THE
TITLE OF INVENTION: EXPRESSION OF TRANSGENES IN NEURONS OF THE MOUSE FOREBRAIN
NUMBER OF SEQUENCES: 8
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                        2;
                    Score 50; DB 12; Length 1743; Pred. No. 1.3e+02; 1; Mismatches 7; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8; Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/969,137 FILING DATE: 12-NOV-1997 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.6%; Score 49; 44.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: COOPER AND DUNHAM
STREET: 1185 AVENUE OF THE AMERICAS
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0575/52776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 269, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
                                                                                                                                                                                                           Sequence 3, Application US/08969137
Patent No. US20010018207A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INCOMATION:
NAME: WHITE, JOHN P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                    37.38;
Query Match
Best Local Similarity 44.4°,
Best Local Similarity 40.4°,
                                                                                                            293 CCTGGCCATGCT--CTCC 308
                                                                                      3 CCNGGCSSKWCRDHARCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CCNGGCSSKWCRDHARCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITED STATES
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: CDNA
US-08-969-137-3
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                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NEW YORK
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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US-08-969-137-3
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Smith, Victoria

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C1
                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/052,586 CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/07886
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-37
PRIOR FILING DATE: 1998-03-37
PRIOR FILING DATE: 1998-03-37
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CURRENT FLILIG DATE: 2002-01-15

PRIOR PELICATION NUMBER: 60/059263

PRIOR PILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-28

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PR FILING DATE: 1997-10-31

PR FILING DATE: 1997-11-13

PR APPLICATION NUMBER: 60/066120

PR FILING DATE: 1997-11-21

PR FILING DATE: 1997-11-24

PR FILING DATE: 1997-11-24

PR PELING DATE: 1997-11-24
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FILING DATE: 1998-04-01
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FILING DATE: 1997-12-12
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APPLICATION UNMBER: 60/068017
FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/077450
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PTILING DATE: 1997-10-29
PTILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063870
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APPLICATION NUMBER: 60/069870
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Watanabe, Colin K. Wood, William I.
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                                                            Zhang, Zemin
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/086023
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-22
PRIOR PLING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086486
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087098
PRIOR PILING DATE: 1998-05-28
                                               R APPLICATION NUMBER: 60/081195
DR FILING DATE: 1998-04-09
DR FILING DATE: 1998-04-15
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/082568
DR FILING DATE: 1998-04-21
DR APPLICATION NUMBER: 60/082569
DR FILING DATE: 1998-04-21
DR APPLICATION NUMBER: 60/08259
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DR APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087609
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/088029
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FILING DATE: 1998-05-15
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APPLICATION WINBER: 60/084640
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
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APPLICATION NUMBER: 60/085573
FILING DATE: 1998-05-15
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FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/083495
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/084366
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APPLICATION NUMBER: 60/084414
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APPLICATION NUMBER: 60/084639
                 APPLICATION NUMBER: 60/081070
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FILING DATE: 1998-04-08
                                   FILING DATE: 1998-04-08
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APPLICANT: Algate, Paul Adate, Paul Adate, Paul Adate, Paul Adapticant: Algate, Paul Adate, Paul Adate
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OTHER INFORMATION: EXPRESSED IN BLAIN, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6

10S-09-864-761-41823
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                                   PRIOR APPLICATION NUMBER: GB 2425.6
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00664
PRIOR PPLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00669
PRIOR PRIOR DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00663
PRIOR PPLING DATE: 2001-01-30
PRIOR PPLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00663
PRIOR PPLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PPLING DATE: 2001-01-30
PRIOR PPLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PPLING DATE: 2001-01-30
PRIOR PPLING DATE: 2001-01-30
PRIOR PPLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234, 687
PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234, 687
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 69/774, 203
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 69/774, 203
PRIOR PLING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN PLACI
OTHER INFORMATION: EXPRESSED IN BRAII
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Publication No. US20020198362A1
GENERAL INFORMATION:
                       APPLICATION NUMBER: GB 24263.6
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Best Local Similarity 41.2.
The Conservative
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FEATURE:
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                       PRIOR
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aconica -X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FULLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-08-03
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38.9%; Pred. No. 1.4e+02;
Live 1; Mismatches 10; Indels
                                                                                                 PRIOR FILING DATE: 1998 -06-05
PRIOR PELING DATE: 1998 -06-05
PRIOR APPLICATION NUMBER: 60/088326
PRIOR APPLICATION NUMBER: 60/088655
PRIOR PILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08873
PRIOR APPLICATION NUMBER: 60/08811
PRIOR PELING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-10
PRIOR PAPLICATION NUMBER: 60/08824
PRIOR PELING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-11
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Patent No. US20020048763A1
                                   FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089105
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PRIOR FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/088212
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PRIOR FILING DATE: 1998-06-17
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Best Local Similarity 38.99
Matches 7; Conservative
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Length 60;
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43.8%; Pred. No. 20;
tive 3; Mismatches
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
NUMBER: 0F SEQ ID NOS: 9597
SOFTWARR: FASLEGG for Windows Version 3.0
SEQ ID NO 1921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)...(60)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-1921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.1
Best Local Similarity 43.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 SSSCSARWCL--GRCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: variant
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/796, 692
CURRENT FILING DATE: 2001-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR PLICATION NUMBER: 60/190, 479
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PLICATION NUMBER: 60/200, 303
PRIOR FILING DATE: 2000-04-28
PRIOR PLICATION NUMBER: 60/200, 303
PRIOR PLICATION NUMBER: 60/200, 999
PRIOR FILING DATE: 2000-05-01
PRIOR PLICATION NUMBER: 60/200, 999
PRIOR FILING DATE: 2000-05-01
PRIOR PLICATION NUMBER: 60/200, 999
PRIOR FILING DATE: 2000-05-01
PRIOR PLICATION NUMBER: 60/202, 084
PRIOR PLICATION NUMBER: 60/202, 903
PRIOR PLICATION NUMBER: 60/202, 903
PRIOR PLILNG DATE: 2000-05-01
PRIOR PLILNG DATE: 2000-05-04
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                        PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR PRILOR DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
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; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-1494
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Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 NGGCSSKWCRDHARCC 20
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US-09-796-692-1921
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LENGTH: 60
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Search completed: January 10, 2003, 08:41:22 Job time: 118.087 secs
                                                                                                                                                                                TYPE: PRT
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COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC TITLE OF INVENTION: NUCLEAR REGULATORY FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 VDGGQVNDRDYMERNKIDVNE----VRSRAQGCCAGERGLGQGCPGSACVSRSHATWARC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 LDGDQPADRP-AERMQDDISSDEHPLFDKRQNCCNG-----GCSSKWC--RDH---ARC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 SAIPVTTISPAHHPHHH-----SHP-----ASCCHGHQRQXSKDHRHLCCG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 TALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCSSKWCRDHAR-CCG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.8%; Score 58; DB 10; Length 312;
Best Local Similarity 27.3%; Pred. No. 31;
Matches 15; Conservative 7; Mismatches 19; Indels 14;
                                                                                                                                                                                                                                                                                                                                                              13.8%; Score 58; DB 10; Length 271; 33.3%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies CURENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: CT/US00/05882
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PLILNG DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-745-763-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: UTSD:695US
CURRENT APPLICATION NUMBER: US/10/029,217A
REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1351, Application US/09925301
Patent No. US20020052308A1
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                                                TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                     LENGTH: 271 amino acids TYPE: amino acid
                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1351
LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-925-301-1351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCNGGCSSKWCRDHA 70
                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                      13.8%; Score 58; DB 9; Length 3907;
44.4%; Pred. No. 4.4e+02;
tive 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.7%; Score 57.5; DB 10; 26.6%; Pred. No. 7.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR PELICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 60/257,761
PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 212, Application US/09894882 Patent No. US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIncosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                          Best Local Similarity 44.49
Matches 8; Conservative
                                                                      NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                ORGANISM: Mus musculus
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50 ECCG 53
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SOFTWARE: Pate
SEQ ID NO 212
                                                                                                                       SEQ ID NO 24
LENGTH: 3907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 PADRPAERMQDDISSDEHPLFDKRQNCCN--GGCSSKW-----CRDHARCC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.9%; Score 58.5; DB 10; Length 621; 30.4%; Pred. No. 56;
                                                                                                                                                                                         APPLICAMT ROSEN et al.
APPLICAMT ROSEN et al.
TITLE OF INVENTION NUCleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 607/US00/05882
PRIOR FILING DATE: 1090-03-08
PRIOR FILING DATE: 1990-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09804898
Patent No. US20020045264A1
GENERAL INFORMATION:
APPLICANT: DINFORMATION:
APPLICANT: XIAO, WEIDONG
TITLE OF INVENTION: PRODUCTION OF CHIMERIC CAPSID VECTORS
FILE REFERENCE: 102182-14
CURRENT APPLICATION NUMBER: US/09/804,898
PRIOR APPLICATION NUMBER: 60/189,110
PRIOR FILING DATE: 2000-03-14
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US-09-749-637A-86
Sequence 86, Application US/09749637A
Patent No. US20020173449A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                              Sequence 1416, Application US/09925301
Patent No. US20020052308A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4621 CCGGCCTTTGC----CCG 4634
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 47.4.
Best Conservative
9, Conservative
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; ORGANISM: Homo sapiens
US-09-925-301-1416
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Best Local Similarity
Matches 17; Conserva
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66 SECADNLKCC 75
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                                                                                                        US-09-925-301-1416
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US-09-804-898-2
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                                                                                   RESULT 9
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Query Match
Best Local Similarity 28.0%; Pred. No. 7.3;
Matches 21; Conservative 9; Mismatches 21; Indels 24; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 KLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPL------FDKR---- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                       APPLICANT: Warkins, Marchael
APPLICANT: Warkins, Marchael
APPLICANT: McIntosh, J. Michael
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Robert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
FILE REPERENCE: 2314-227
CURRENT APPLICATION NUMBER: US/09/749,637A
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/213,412
PRIOR APPLICATION NUMBER: US 60/219,440
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE PALENTING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SSEQ ID NOS: 409
SSEQ ID NOS: 409
SSEQ ID NOS: 409
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STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collins-Racie, Lisa A.
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Sprunger, Suzanne A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCoy, John M.
LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-745-763-77; Sequence 77, Application US/09745763; Patent No. US20020065394A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treacy, Maurice
Spaulding, Vikki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jacobs, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCES: 219
Cartier, G. Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Conus pennaceus
                            Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 EACNIITONCCDGKC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 -----0NCCNGGC 61
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24; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALO1
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.0%; Score 59; DB 10; Length 1200; 47.4%; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides TITLE OF INVENTION: and Polynucleotides FILE REFERENCE: GP-707440SB
                           28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                  8 GVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDE----
Best Local Similarity 25.3%; Pred. No. 54;
Matches 21; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 99;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/826,508 CURRENT FILING DATE: 2001-04-05 NUMBER OF SEQ ID NOS: 40 SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1361, Application US/09925300 Patent No. US20020151681A1
                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09826508
Patent No. US20010025099A1
GENERAL INFORMATION:
APPLICANT: Nabil Elshourbagy
APPLICANT: Lisa Vawter
                                                                                                                                                     50 FDKRQNCCNGGCSSKWCRDHARC 72
                                                                                                                                                                                65 FQHFQN--NG--SLVWCQNHKQC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 CCNGGCSSKWCRDHARCCG 74
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Best Local Similarity 47.4
Matches 9; Conservative
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1361
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LENGTH: 1200
                                                                                                                                                                                                                                                                 RESULT 7
US-09-826-508-3
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APPLICANT: PETIT, CHRISTINE
APPLICANT: SOUSSI-YANICOSTAS, NADIA
APPLICANT: ARADELIN, JEAN-PIERRE
APPLICANT: ROGGON, GENEYTEVE
APPLICANT: ROGGON, GENEYTEVE
APPLICANT: ARADEL, JEAN-CLAUDE
APPLICANT: ARAZIE, JEAN-CLAUDE
TITLE OF INVENTION: THERAPEUTIC COMPOSITION COMPRISING KAL PROTEIN AND USE
TITLE OF INVENTION: OF THE KAL PROTEIN FOR THE TREATMENT OF RETINAL, RENAL,
TITLE OF INVENTION: NEGRONAL AND NEURAL INJURY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.2%; Score 59.5; DB 9; Length 319; 26.7%; Pred. No. 22; tive 9; Mismatches 17; Indels 2
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                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUBBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUBBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 5612
                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILE REFERENCE: 0660-0151-0XPCT
CURRENT APPLICATION NUMBER: US/10/119,714
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US/09/319,236
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VOR: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/10119714
; Patent No. US20020123467A1
                                                         APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MAYASHI, MIKIRO
APPLICANT: GCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NACHIRO
APPLICANT: SENOH, MAKHIRO
Publication No. US20020197605A1
                GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.79
Watches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 ASLMLEKLLKDKGKN 193
                                                                                                                                                                                                                   IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 ----EHPLFDKRQN 55
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US-10-119-714-1
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LENGTH: 679
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US-10-119-714-1
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APPLICANT:
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083545
FILING DATE: 1998-04-29
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FILING DATE: 1998-04-09
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FILING DATE: 1998-04-14
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FILING DATE: 1998-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/084627 PRIOR FILING DATE: 1998-05-07
                                                                                                                                          APPLICATION NUMBER: 00/065846
FILING DATE: 1997-11-12
FILING DATE: 1997-11-17
FILING DATE: 1997-11-17
FILING DATE: 1997-11-17
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069278
FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069334
FILING DATE: 1997-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-12-16
APPLICATION NUMBER: 60/072320
FILING DATE: 1998-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/074086
FILING DATE: 1998-02-09
APPLICATION NUMBER: 60/074092
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APPLICATION NUMBER: 60/078910
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FILLING DATE: 1998-02-27
APPLICATION NUMBER: 60/079728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/081203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/081818
                             FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063735
FILING DATE: 1997-10-29
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APPLICATION NUMBER: 60/064248
FILING DATE: 1997-11-03
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APPLICATION NUMBER: 60/066453
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066511
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APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/069212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
                                                                           APPLICATION NUMBER: 60/063738
                                                                                       FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063755
                                                                                                                                                                                                APPLICATION NUMBER: 60/065186 FILING DATE: 1997-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/069694
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                APPLICATION NUMBER: 60/063733
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1997-10-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 189;
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US-09-738-626-5612
; Sequence 5612, Application US/09738626
A AFFLANCE DATE: 1998-05-0/
R APPLICATION NUMBER: 60/085149
/R FILING DATE: 1998-05-12
/R APPLICATION NUMBER: 60/085323
/R APPLICATION NUMBER: 60/085323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 19/98-06-11
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
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PRIOR FILING DATE: 1938-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-66-24
PRIOR PELICATION NUMBER: 60/090863
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PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/087106
FILLING DAPE: 1988-05-28
APPLICATION NUMBER: 60/088026
FILLING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/086414
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/086430
FILING DATE: 1998-05-22
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
FILING DATE: 1998-05-15
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/085339
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FILING DATE: 1998-05-15
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FILING DATE: 1998-06-10
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Best Local Similarity 25.8%
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                    4 MSKLGVLLTVCLLLFPLTALPLDGD------QPADRPAER--MQDDISSDEHP---- 48
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14.4%; Score 60.5; DB 9; Length 189;
Best Local Similarity 25.8%; Pred. No. 9.6;
Matches 23; Conservative 12; Mismatches 31; Indels 2
                                                                                                                                                                                                       Length 104;
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US-09-965-528-14
                                                                                                                                                                                                    Query Match
14.5%; Score 61; DB 10; Length 10;
Best Local Similarity 29.6%; Pred. No. 4.5;
Matches 29; Conservative 5; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                             49 -----LFDKRQNCCNGGCSS--KWCRDHARCCGR 75
                                                                                                                                                                                                                                                                                                                                                                                                                             59 CGREAFRVTLQDGRQGCVSVGNQSLLDWLKGHKDLCPR 96
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PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/157,508
PRIOR APPLICATION NUMBER: 60/157,508
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL PROGRAM
                                                                                                                 ; TYPE: PRT
; ORGANISM: Molluscum contagiosum virus
US-09-920-897-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09965528 Publication No. US20020187523A1 GENERAL INFORMATION:
CURRENT FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: INCYTE GENOMICS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YUE, Henry
LAL, Preeti
BUREORD, Neil
BANDMAN, Olga
BAUGHM, Mariah R.
AZIMZAI, Yalda
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                      NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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LENGTH: 189
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CURRENT APPLICATION NUMBER: US/10/028,072
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PRIOR FILLING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/04911
PRIOR PAPLICATION NUMBER: 60/056974
PRIOR PAPLICATION NUMBER: 60/059113
PRIOR PAPLICATION NUMBER: 60/059113
PRIOR PAPLICATION NUMBER: 60/059115
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059127
PRIOR PILING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-32
                       Sequence 232, Application US/10028072 Publication No. US20030004311A1
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FILING DATE: 1997-09-24
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APPLICATION NUMBER: 60/063550
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APPLICATION NUMBER: 60/063561
FILING DATE: 1997-10-28
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PRIOR APPLICATION UNDRER: 60/05935
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
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PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
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APPLICATION NUMBER: 60/063329
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                                                                                                                                                                                                                                            Gerritsen, Mary E.
Goddard, Audrey
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                                                                                               APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Gurney, Austin L.
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Filvaroff, Ellen
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TITLE OF INVENTION:
                                                                       GENERAL INFORMATION:
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JS-10-028-072-232
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OM protein - protein search, using sw model

January 10, 2003, 08:33:07; Search time 116.087 Seconds (without alignments) 12.534 Million cell updates/sec Run on:

US-09-910-009A-210 420 Perfect score: Title:

1 GSMMSKLGVLLTVCLLLFPL......CCNGGCSSKWCRDHARCCGR 75 Sequence:

Scoring table:

118974 seqs, 19401057 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Published_Applications_AA:* Database :

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SUMMARIES

Description	Sequence 1, Appli	Sequence 4, Appli	Sequence 14, Appl	Sequence 232, App	Sequence 5612, Ap	Sequence 1, Appli	Sequence 3, Appli	Sequence 1361, Ap	Sequence 1416, Ap	Sequence 2, Appli	Sequence 86, Appl	Sequence 77, Appl	Seguence 1351, Ap	Sequence 24, Appl	Sequence 212, App	Sequence 609, App	Sequence 2, Appli	Sequence 61, Appl	Sequence 62, Appl
OI OI	US-10-096-961-1	US-09-920-897-4	US-09-965-528-14	US-10-028-072-232	US-09-738-626-5612	2 US-10-119-714-1	0 US-09-826-508-3	0 US-09-925-300-1361	0 US-09-925-301-1416	0 US-09-804-898-2	US-09-749-637A-86	0 US-09-745-763-77	0 US-09-925-301-1351	US-10-029-217A-24	0 US-09-894-882-212	0 US-09-925-302-609	0 US-09-950-046A-2	US-09-950-933A-61	US-09-950-933A-62
% Query Match Length DB	2211 9	104 10	189 9	189 9	319 9	679 13	1200 10	137 10			80 9							108 9	117 9
% Query Match L	14.8	14.5	14.4	14.4	14.2	14.0	14.0	13.9	13.9	13.9	13.8	13.8	13.8	13.8	13.7	13.7	13.7	13.6	13.6
Score	62	61	60.5	60.5	59.5	59	59	58.5	58.5	58.5	58	58	58	58	57.5	57.5	57.5	57	23
Result No.	1	2	٣	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 8, Appli Sequence 5, Appli Sequence 6, Appli Sequence 470, App Sequence 274, App Sequence 71, Appl Sequence 11, Appl Sequence 15, Appl Sequence 63, Appl Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 39, Appli Sequence 39, Appli Sequence 36, Appli Sequence 39, Appli	Sequence 4912, App Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 3, Appli Sequence 56, Appl Sequence 246, Appl Sequence 246, Appl Sequence 246, Appl Sequence 44, Appl
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ALIGNMENTS

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Sequence 1, Application US/10096961
Patent No. US200201555721
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE REPERENCE: CLOO00449DIV
CURRENT APPLICATION NUMBER: 08/10/096,961
PRIOR APPLICATION NUMBER: 09/232,632
PRIOR APPLICATION NUMBER: 09/232,632
PRIOR APPLICATION NUMBER: 09/38,884
PRIOR APPLICATION NUMBER: 09/38,884
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SOFTYARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2211
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Matches 10; Conservative
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ORGANISM: Homo sapien
US-10-096-961-1
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US-09-920-897-4

Sequence 4, Application US/09920897

Patent No. US/2002000489A1

GENERAL INFORMATION:
APPLICANT: Paslin, David A.
TITLE OF INVENTION: ATOPIC DERMATITIS METHOD
FILE REFERENCE: 17761-702

CURRENT APPLICATION NUMBER: US/09/920,897